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2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
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6: geneseqp2003bs:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
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## ALIGNMENTS

#### RESULT 1 AAE06683 Homo Human vanilloid receptor VR3 isoform, 16-OCT-2001 AAE06683; AAE06683 standard; protein; Human; sapiens. (first entry) 742 Ž VR3A+B+.

postmastectomy pain; complex regional pain syndrome; arthritis; rheumatoid arthritis; osteoarthritis; ulcer; neurodegenerative disease; chronic obstructive pulmonary disease; irritable bowel syndrome; psoriasis; central nervous system disease; CNS; cancer; intestinal tract disorder; VR3A+B+. iuman; vanilloid receptor; VR3; inflammatory condition; analgesic; intractable pain; postherpetic neuralgia; diabetic neuropathy; asthma;

WO200158945-A1

16-AUG-2001.

01-FEB-2001; 2001WO-US003456.

08-FEB-2000; 2000US-00500123.

(ORTH ) ORTHO-MCNEIL PHARM INC

Dubin AE,

Huvar A,

Glass CA,

Erlander MG

N-PSDB; 2001-488969/53. DB; AAD12793.

cancers arthritis and pain. New human VR3 receptor useful for the treatment of disorders including

Claim 11; Fig 8; 104pp; English.

The patent relates to human vanilloid receptor VR3 polynucleotide and polypeptide. Three isoforms of VR3 namely VR3A+B-, VR3A-B- and VR3A+B+ have also been disclosed. The VR3 polypeptide is used to identify its modulators which are useful for the treatment of inflammatory conditions and for use as analgesics for intractable pain associated with postherpetic neuralgia, diabetic neuropathy, postmastectomy pain, complex regional pain syndromes, arthritis (e.g. rheumatoid and osteoarthritis), ulcers, neurodegenerative diseases, asthma, chronic

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Human vanilloid receptor-related channel
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neurological disease; inflammatory disease; cancer; Alzheimer's d Parkinson's disease; asthma; rheumatoid arthritis; liver disease; hepatitis; cirrhosis; kidney disease; glomerulonephritis. Human; calcium entry modulator; CD4536; CD5842; intracellular calcium; cer; Alzheimer's diseas disease;

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US2004009537-A1
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13-JAN-2003;
2003US-00342844
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15-JAN-2004

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11-JAN-2002; 2002US-0347459P.
02-AUG-2002; 2002US-0401171P.
20-AUG-2002; 2002US-0405678P.
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N-PSDB; ADI81605. 2004-090465/09

cancer), comprises monitoring Identifying an agent that modulates intracellular calcium levels, useful for treating diseases associated with calcium dysregulation (e.g. cancer), comprises monitoring the effects of the agent on store-operated calcium entry.

Disclosure; SEQ ID NO 76; 55pp; English

cc intracellular calcium comprises monitoring the effects of the agent on cortecilular calcium entry comprising contacting one or more test cells cor their portion comprising one or more proteins that is (are) at least cabout 35% homologous to the protein encoded by Drosophila gene CG4536 or CG CG5842 over at least about 40% of the encoded protein (and that provides Cf for store-operated calcium entry with a test agent), where the portion of the cell comprises the proteins, monitoring the effect(s) of the test compound on store-operated calcium entry and identifying a test agent as an agent if it has an effect on store-operated calcium entry. Also cincluded are a method of modulating store-operated calcium entry comprising modulating the level of, expression of, activity of or compound on store-operated calcium entry. Where the protein is a cell that has altered store-operated calcium entry, where the protein is at least about 35% cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the protein and that provides for CG Estat about 40% of the protein sate least about 40% or CG5842 cover at least about 40% of the continued above, thus, and the protein and that provides appearing as the protein does not contain the con The invention relates to identifying an agent that modulates

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                                                             Human; vanilloid receptor 3; VR3; inflammation; arthritis; psoriasis; wound healing; analgesic; vulnerary; antiallergic; gene therapy; neuropathic pain; rhinitis; pruritus; bladder dysfunction; cluster headache; capsaicin-sensitive ion channel disorder.
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Location/Qualifiers
238. .269
/label= Ankaryn_repeat
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GDGRPNIRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP

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MADSSEGPRAGPGEVAELPGDESGTPGGEAPPLSSLANLFEGEDGSLSPSPADAGRPAGP

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Query Match
Best Local S
Matches 736
                                                                    Vanilloid receptor protein and its DNA are useful for identifying compounds which modulate vanilloid receptors in human tissues, which are useful for treating various disease states, including neuropathic pain, inflammation, arthritis, rhinitis, pruritus, bladder dysfunction, cluster headache, wound healing and psoriasis. Vanilloid receptor DNA is useful as standard or reagent in diagnostic immunoassays, as targets for pharmaceutical screening assays and also in gene therapy. Vanilloid receptor protein is useful for detecting the presence of anti-vanilloid receptor derived polypeptide in test samples. Vanilloid receptor sectived polypeptide in test samples. Vanilloid receptor sections are useful for detecting vanilloid receptor polypeptides, for screening for diseases or conditions associated with abnormal vanilloid receptor production, treating disorders involving capsaicin-sensitive ion channels and as diagnostic markers
                                                     Sequence
                                                                                                                                                                                                                                                                                           Novel human vanilloid receptor gene and encoded polypeptides for identifying compounds that modulate vanilloid receptors in human tissues and for treating inflammation, arthritis, psoriasis and wound healing.
                                                                                                                                                                                                                                                                           Claim 18;
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-335930/35.
N-PSDB; AAD05107.
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    Local Simi
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515. .53
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              99.2%; Score 3829;
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                                                                             WPI; 2001-596911/67.
                                                                                                                                    Curtis RAJ,
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                                                       AAI66972, AAI66973
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Nucleic

acid

encoding

human

not

channels referred to as Vanilloid

and pain disorders. receptor 3 (VR-3) and VR-5, useful for screening modulators of VR-3 or VR -5 and for treating calcium homeostasis related disorders (e.g. dementia)

Claim 13; Fig 2A-C; 167pp; English.

The invention provides nucleic acid encoding human ion channels referred to as Vanilloid receptor 3 (VR-3) and VR-5. The VR-3 or VR-5 proteins can be used to screen for naturally occurring VR-3 or VR-5 ligands or for drugs or compound which modulate VR-3 or VR-5 activity. The VR-3 or VR-5 proteins and their modulators (e.g. antisense nucleic acids and anti-VR antibodies) are useful for treating disorders characterized by insufficient or excessive production of VR-3 or VR-5. These disorders are calcium homeostasis related disorders (Alzheimer's disease, dementia, parkinson's disease), pain disorders (diabetic neuropathy, rheumatoid arthritis) and/or cellular growth and/or proliferation disorders (e.g. cancer). Numerous other examples of these disorders are given in the specification. The present sequence represents the human VR-5

Sequence 871 AA;

DB 4.

Length

871;

S 맑 15 뮹 Š 밁 S g 8 Ş 밁 Ś 밁 Š 밁 Ś 맑 S 밁 \$ 뮍 5 밁 Query Match
Best Local Similarity 100.
Matches 736; Conservative 121 121 421 361 361 301 301 241 241 181 181 541 481 481 421 541 61 661 61 щ GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELFLSLAACTNQPHI KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL LSSLDTCGEEASVLEIL VYNSKI ENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD UNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS ALHTATERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV AMVIETLTAYYOPLEGT:PPYPYRTTVDYLRLAGEVITLFTGVLFFETNIKDLFMKKCPGV LSSIDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 99.2%; Score 3829; DI; Pred. No. 0; 0; Mismatches 0 0; Indels 0 Gaps 120 600 540 540 480 420 360 360 300 300 240 180 180 60 720 600 480 420 660 660

В S

721 721

TVGQVSKESKHIWKLQ TVGQVSKESKHIWKLQ

736 736

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RESULT 5
AAU74935
ID AAU74935
AAU74937
AX AAU7
XX AAU7
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DT 23-A
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                                                                                                                                                                                                                                                                                The present invention relates to a new polypeptide that has a sequence CC 871 amino acids (AAU74935) or 662 amino acids (AAU74936) long, or their variants, as defined in the specification. The polypeptide of the CC invention is deduced from a human nucleic acid 2749 base pairs (ABK14002) CC respectively. The polypeptides of the invention, which are human CC vanilloid receptor-like (VRL) proteins, are used to identify specific CC modulators that are potentially useful for treating pain (of any origin), CC neurodegeneration, stroke, inflammation, asthma, allergy, urogenital CC disorders, incontinence, hypo- or hyper-tension and perivascular disease. The molecules of the invention can also be used to raise specific CC antibodies. The nucleic acid that encodes the polypeptide of the invention is useful for recombinant production of the protein and for preparing transgenic animal models. The polypeptide, antibody and nucleic acid of the invention are also useful as diagnostic agents for CC acid sequence represents the human vanilloid receptor-like protein 2a (CC (VRL-2a) of the invention
                                                                                                                 Query Match
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Matches 736
                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                       standard;
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Human VR4 protein SEQ ID NO:2.

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XX Homo
XX Y YO2-M
YD 02-M
XX XX Y 25-C
XX Human; VR4; vanilloid 4 receptor; receptor; osteopathic; antirheumatic; antiathritic; vulnerary; analgesic; gene therapy; cartilage; bone; larynx; auditory canal; intravertebral disc; ligament; tendon; joint capsule; bone development disorder; osteoporosis; osteoarthritis; joint destruction; rheumatoid arthritis. WO200234280-A2 Homo sapiens

25-OCT-2001; 2001WO-GB004739

02-MAY-2002

25-OCT-2000; 2000GB-00026114

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of vanilloid 4 receptor polypeptide/polynucleotide, a modulator of the polypeptide or an antisense polynucleotide to the polynucleotide, manufacture of a medicament for treating cartilage and/or bone disease
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                 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG
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NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG
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                                                                                                                                                                                                                  The present invention relates to a polypeptide of ion channel family polypeptides, vanilrep4 (VR4). The peptides are useful for treating pain (e.g. chronic pain, neuropathic pain, post-operative pain, rheumatoid arthritic pain), neuralgia, neuropathies, algesia, nerve injury, ischemia, neurodegeneration, stroke, incontinence, inflammatory disorders, irritable bowel syndrome, diabetes or obesity. Fragments of the protein are useful for producing full-length polypeptides by peptide synthesis therefore the variants may also by employed as intermediate for producing full-length polypeptide. The proteins are also useful for identifying agonists or antagonists of peptide activity and expression. The peptide is useful as disease by detecting mutations in the associated gene, and is also useful for chromosome localization studies and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vanilrep4; VR4; Analgesic; cerebroprotective; antiinflammatory;
antidiabetic; anorectic; vasotropic; uropathic; ischemia;
neurodegeneration; inflammatory disorder; irritable bowel syndrome;
expression studies. The peptide is useful for producing transgenic animals, which include knock-in animals (in which an animal gene is replaced by human equivalent within the genome of the animal), useful drug discovery process, for target validation, where the compound is specific for human target. Peptides and Ab is useful for configuring screening methods for detecting the effect of added compounds on the production of mRNA in cells. The peptides are useful as vaccines for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptide of ion channel family polypeptides, designated vanilrep4, useful as a vaccine for inducing immune response against diseases suc neuropathies, algesia, nerve injury, ischemia, stroke, incontinence,
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13-JUN-2001; 2001US-0297835P.
22-JAN-2002; 2002US-0351238P.
29-JAN-2002; 2002US-0352914P.
12-FEB-2002; 2002US-0357161P.
15-MAY-2002; 2002US-0381086P.
16-MAY-2002; 2002US-0381739P.
                                                                                                                                                                                                                                                                           TRPV7; TRPV4; VRL3; OTRPC4; TRPM8; TRPX; trkA+; inflammation; skin disorder; cancer; analgesic; antiinflammatory; dermatolo cytostatic.
                                                                                                                                              Patapoutian
                                                                                                                                                           (NOVS )
                                                                                                                                                                                                                         13-ЛИМ-2002;
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DB; ADG32561.
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                                                                                                                                             Bevan
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New isolated TRPV3, TRPV4 or TRPM8 vanilloid receptor nucleic molecule and polypeptides, useful for the diagnosis and treatm disorders such as pain, inflammation, skin diseases and cancer treatment cancer. O.

SEQ ID NO 17; 197pp; English.

acids and encoded proteins thereof. Specifically, it refers to certain members of the VR family that are involved in pain perception, in particular, TRPV3 (previously known as VRLS, VRLX, VR4 & TRPV1), TRPV4 (previously known as VRL3 & OTRPC4) and TRPM8 (previously known as TRPX). Furthermore, this invention includes trkA+ pain specific genes expressed in the sensory neurons of the dorsal root ganglia. Accordingly, such compositions can be useful for the diagnosis, treatment and prevention of pain, inflammation, skin disorders and cancer, and so exhibit analgesic, antiinflammatory, dermatological and cytostatic activities. This polypeptide sequence is the human TRPV4 protein of the invention. invention relates to novel vanilloid receptor (VR) related nucleic and encoded proteins thereof. Specifically, it refers to certain

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VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLLKCARLFPDS
                                                  ALHIAI ERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
                                                                                                TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT
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                                                                                                                                                KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL
                                                                                                                                                                                 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN
                                   ALHIAI ERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
                                                                                   TDEEFREPSTGXTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT
                                                                                                                                                                                                                                                                                99.2%; Silarity 100.0%; Conservative 0;
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The invention relates to a purified protein (I) that promotes type II collagen expression. Also disclosed is an isolated polynucleotide encoding (I), a recombinant vector comprising the polynucleotide and gene therapeutic agent comprising the recombinant vector as an active
                                                                                                                                                                                                                                                                                                                                                                                                                                  16-APR-2002;
19-APR-2002;
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                                                                                                                           Claim 1; SEQ
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                                                                                                                                                                  purified protein that promotes type II collagen expression, useful preventing and treating a cartilage disease, e.g. osteoarthritis, tilage defect, or rheumatoid arthritis.
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22-APR-2004

(first entry)

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Matches 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ingredient. The proteins, genes, agents and methods are useful for preventing and treating a cartilage disease, e.g. osteoarthritis, cartilage defect, or rheumatoid arthritis. The current sequence represents a human protein that promotes type II collagen express
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                                                          RDSETESTELLDLEKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE
                                                                                                                                         NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG
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calcium;

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cc or their portion comprising one or more proteins that is (are) at least about 35% homologous to the protein encoded by Drosophila gene CG4536 or CG5842 over at least about 40% of the encoded protein (and that provides CC for store-operated calcium entry with a test agent), where the portion of the cell comprises the proteins, monitoring the effect(s) of the test compound on store-operated calcium entry and identifying a test agent as an effect on store-operated calcium entry. Also CC included are a method of modulating store-operated calcium entry. Also CC included are a method of modulating store-operated calcium entry. Of or comprising modulating the level of, expression of, activity of or comprising modulating the protein in a cell that has altered store-operated calcium entry. Also CC included are the protein encoded by Drosophila gene CG4536 or CG5842 over at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila gene CG4536 or CG5842 cover at least about 40% of the encoded by Drosophila protein and that provides for CG5842 cover at least about 40% of the encoded by Drosophila proteins as provides for CG5842 cover at least about 40% of the Evolution of the Ev
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02-AUG-2002;
20-AUG-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying an agent that modulates intracellular calcium levels, useful for treating diseases associated with calcium dysregulation (e.g. cancer), comprises monitoring the effects of the agent on store-operated
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MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP

Matches

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Similarity

99.2%;

Score 3829; D; Pred. No. 0; O; Mismatches

DB

Length Indels

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13-JAN-2003;

2003US-00342844

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CC intracellular calcium entry comprising ontacting one or more test cells or their portion comprising one or more proteins that is (are) at least cor their portion comprising one or more proteins that is (are) at least cor about 35% homologous to the protein encoded by Drosophila gene CG4536 or CC G5842 over at least about 40% of the encoded protein (and that provides CC included are a method of modulating, monitoring the effect(s) of the test agent if it has an effect on store-operated calcium entry and identifying a test agent as compound on store-operated calcium entry also compound on store-operated calcium entry. Also compound on store-operated calcium entry (comprising modulating the level of, expression of, activity of or comprising modulating the level of, expression of, activity of or compound or interactions of a protein in a cell that has altered store-operated calcium entry, where the protein is at least about 35% noncloquals to the protein encoded by Drosophila gene CG4536 or CG5842 over at least about 40% of the encoded protein and that provides for store-operated calcium entry, and where store-operated calcium transport comprising molecules involved in modulating sene CG4536 or CG5842 over at least about 40% of the encoded protein and that provides for comprising a molecule that interacts with the protein mentioned above, thus, it is protein shown that protein that provides for store-operated calcium transport comprising molecules involved in modulating store-operated calcium transport comprise the protein are selected from ion transport comprise the protein selection. These may be used in treating comprise the protein selection of the two above mentioned drosophila proteins.

CC glomerulonephritis). The present sequence represents an 
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02-AUG-2002;
20-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying an agent that modulates intracellular calcium levels, useful for treating diseases associated with calcium dysregulation (e.g. cancer), comprises monitoring the effects of the agent on store-operated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 78; 55pp; English
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 871 AA;
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                                                                                                                                                                                                                                                                                            736;
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) STAUDERMAN
) VELICELEBI
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                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                   GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
                                                                                                                                                                                                                                  WADSSEGPRAGPGEVABLPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
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                                                               KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLITHKKRI 180
  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT
                                                                                                                              GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN
                                                                                                                                                                                                                MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP
                                         KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLFFLLTHKKRL
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ROOS J. STAUDERMAN VELICELEBI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; calcium entry modulator; CD4536; CD5842; intracellular calcium; neurological disease; inflammatory disease; cancer; Alzheimer's disease; Parkinson's disease; asthma; rheumatoid arthritis; liver disease; hepatitis; cirrhosis; kidney disease; glomerulonephritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human vanilloid receptor-like channel
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02-AUG-2002;
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CC intracellular calcium comprises monitoring the effects of the agent on
CC store-operated calcium entry comprising contacting one or more test cells
CC or their portion comprising one or more proteins that is (are) at least
about 35% homologous to the protein encoded by Drosophila gene CG4536 or
CC G5842 over at least about 40% of the encoded protein (and that provides
CC in store-operated calcium entry with a test agent), where the portion of
CC compound on store-operated calcium entry and identifying a test agent as
CC an agent if it has an effect on store-operated calcium entry
CC included are a method of modulating store-operated calcium entry
CC included are a method of modulating store-operated calcium entry
CC comprising modulating the level of, expression of, activity of or
CC included are a method of modulating store-operated calcium entry
CC comprising modulating the level of, expression of, activity of or
CC included are a method of modulating store-operated calcium entry
CC over at least about 40% of the encoded by Drosophila gene CG4536 or CG5842
CC over at least about 40% of the encoded by Drosophila gene CG4536 or CG5842
CC over at least about 40% of the encoded by Drosophila gene CG4536 or CG5842
CC into the cell is modulated) and method of identifying a molecule that
CC into the cell is modulated and in method of identifying a molecule that
CC into the cell is modulated and method of identifying a molecule that
CC into the cell is modulated and method of identifying a molecule that
CC into the colling into contain the contiguous sequences appearing as
CC identifying molecules involved in modulating store-operated calcium
CC ablieve that intracellular calcium. These may be used in transport
CC diseases associated with calcium dysregulation, such as neurodegenerative
CC diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
CC diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches 736
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homologue of one of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying an agent that modulates intracellular calcium levels, useful
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DB; ADI81587.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hepatitis or cirrhosis) or kidney diseases (e.g. rulonephritis). The present sequence represents an
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                        VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS
                                                                                 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
                                                                                                          ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
                                                                                                                                                                                           TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVILDIAERTGNMREFINSPFRDIYYRGQT
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VNYLTENPHKKADMRRQDSRGNTVLHALVA I ADNTRENTKFVTKMYDLLLLKCARLFPDS
                                                                                                                                                                       TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT
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NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD

Modulating mechanoreception or mechanosensation, for diagnosing, preventing or treating e.g. hearing disorders, HIV or obesity, c administering a vanilloid receptor-related osmotically activated

activated

comprises d channel

2002-599762/64. DB; ABQ79489.

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                                                                                                                                                                                                                       Liedtke W,
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25-OCT-2001;
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2001US-00243568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vanilloid receptor-related osmotically activated channel;
                                                                                                                                                                                                                       Hudspeth
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The invention relates to modulating mechanoreception/mechanosensation in CC a mammal by administering a vanilloid receptor-related osmotically CC activated channel (VR-OAC) polypeptide, its active fragments or portions, CC or by introducing a nucleic acid vector capable of expressing the VR-OAC CC polypeptide. The method of the invention is useful for modulating CC mechanoreception or mechanosensation, for diagnosing, preventing or CC treating e.g. hearing disorders, Human Immunodeficiency virus (HIV), CC obesity, vertigo of labyrinthine origin including motion sickness, CC neurological disorders including ataxia, male infertility, immune CC dysfunction, diabetes mellitus, chronic obstructive lung disorder; CC bronchial asthma, sexual dysfunction, blindness due to corneal or retinal causes, or skin disorders including psoriasis. Other conditions include arterial hypertension, kidney diseases, pain syndromes, Alzheimer's CC disease and other dementias, hydrocephalus, alopecia, baldness and CC cancer. The VR-OAC may be used in detecting or assessing osmotic and cechanical stimuli, or as the facilitating component in translating an osmotic or mechanical stimulus in nano-technological, biosensor or cc biorobotic devices. The current sequence represents the amino acid sequence of human VR-OAC as determined from HEX293 cells. NOTE: The creating these polypeptides which are referred to as SEQ ID's 5, 6, 7, 8 and is criven.
  Query Match
Best Local :
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                                                                      Sequence 871
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ADIBISIT AC ADIBISIT ADIBISI ADIBISIT ADIBISIT ADIBISIT ADIBISIT ADIBISIT ADIBISIT ADIBISIT Ś 멍 Ş 먕 S 문 Human; calcium entry modulator; CD4536; CD5842; intracellular calcium; neurological disease; inflammatory disease; cancer; Alzheimer's disease; Parkinson's disease; asthma; rheumatoid arthritis; liver disease; hepatitis; cirrhosis; kidney disease; glomerulonephritis. 22-APR-2004 ADI81590 ADI81590 standard; protein; 871 13-JAN-2003; 2003US-00342844 15-JAN-2004 US2004009537-A1 601 601 661 661 721 721 vanilloid receptor-related channel protein #1. RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLLMLIALMGE TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC TVGQVSKESKHIWKLQ TVGQVSKESKHIWKLQ 736 RDSETFSTFLLDLFKLTIGMGDI (first entry) A LEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720 720 660 660

11-JAN-2002; 2002US-0347459P. 02-AUG-2002; 2002US-0401171P. 20-AUG-2002; 2002US-0405678P. (ROOS/) (STAU/) VELICELEBI ROOS J. STAUDERMAN Stauderman K, ج 0 Velicelebi

Identifying an agent that modulates intracellular calcium levels, useful for treating diseases associated with calcium dysregulation (e.g. cancer), comprises monitoring the effects of the agent on store-operated entry.

N-PSDB;

2004-090465/09.

ADI81589

Disclosure;

SEQ ID NO

60; 55pp; English

The invention relates to identifying an agent that modulates contracellular calcium comprises monitoring the effects of the agent on contractive calcium entry comprising contacting one or more test cells or their portion comprising one or more proteins that is (are) at least contractive contra

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc into the cell is modulated) and a method of identifying a molecule that comproved the provides for store-operated calcium entry (comprising identifying a complecule that interacts with the protein mentioned above, thus, completely imposed the protein modulating store-operated calcium comparity. The protein does not contain the conciguous sequences appearing as compared that interactly in a modulating, or in identifying agents compressed that modulate, intracellular calcium. These may be used in treating compared that modulate, intracellular calcium. These may be used in treating compared to the modulate of the calcium dysregulation, such as neurodegenerative compared (e.g. Alzheimer's disease or Parkinson's disease), inflammatory compared (e.g. asthma or rheumatoid arthritis), cancer, liver diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases (e.g. hepatitis or cirrhosis) or kidney diseases (e.g. compared the two above mentioned drosophila proteins.
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Best Local S
Matches 735
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                                                                        RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLLNMLIALMGE
                                                                                                                                  TYSIMIQKILFKDLFRFLLYYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC
                                                                                                                                                                                          NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG
                                                                                                                                                                                                                                   AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV
                                                                                                                                                                                                                                                                                                                                                                             NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
                          TVGQVSKESKHIWKLQ 736
                                                      RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE
                                                                                                               TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC
                                                                                                                                                                                                                                                                                               LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC
                                                                                                                                                                                                                                                                                                                      LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC
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Pred. No. 0;
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Best Local Similarity
Matches 735; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-DEC-2001;
11-DEC-2001;
14-MAR-2002;
14-MAR-2002;
12-APR-2002;
12-APR-2002;
22-APR-2002;
24-APR-2002;
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Ma Y,
                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides, useful for expressing recombinant proteins analysis, characterization or therapeutic use, or as markers for in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel
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KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL
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Xue AJ, Wehrman T,
ng D, Chen R, Xu C,
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2002US-0339453P.
2002US-0365091P.
2002US-0365384P.
2002US-0372381P.
2002US-0372615P.
2002US-00128558.
2002US-0376045P.
                                                                                                                                                                                                                                                              Conservative
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Pred. No. 0;
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, Weng G, Zhou l
C, Boyle BJ;
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820 TVGQVSKESKHIWKLQ 835	721 TVGQVSKESKHIWKLQ 736	760 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 819	661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720	700 TYSIMIQKILFKOLFRELLVYLLFMIGYASALVSLINPCANMKVCNEDQINCTVPTYPSC 759	601 TYSIMIQKILEKDLERELLVYLLEMIGYASALVSLLNECANMKVCNEDQTNCTVPTYPSC 660	640 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVEALVLGWMNALYFTRGLKLTG 699	541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600	580 AMVIETLTAYYQDLEGTEPYPYRTTVDYLRLAGEVITLETGVLFFETNIKDLFMKKCPGV 639	481 AMVIETLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLETGVLFEFTNIKDLEMKKCPGV 540	520 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 579	421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVGFYINVVSYLC 480	460 NLEAVLNNDGLSPLMWAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 519	361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420	400 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 459	301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLILKCARLFPDS 360	340 ALHIAIERRCKHYVELLVAQGADVHAQARGRFRQPKDEGGYFYFGELPLSLAACTNQPHI 399	241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300	280 TDEEFREPSTGKTCLFKALLNLSNGRNDTIFVLLDIAERTGNWREFINSFFRDIYYRGQT 339	181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNWRBFINSDFRDIYYRGQT 240

Search completed: December 2, 2004, 22:23:18 Job time : 168 secs

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Minimum
Maximum
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Perfect score:
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Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
       is the number of results predicted by chance to have a ster than or equal to the score of the result being printed,
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3858
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Maximum Match 100%
Listing first 45 summaries
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Sequence 12, Appli Sequence 9, Appli Sequence 25, Appli Sequence 27, Appli Sequence 34, Appli Sequence 34, Appli Sequence 34, Appli Sequence 34, Appli Sequence 44, Appli Sequence 44, Appli Sequence 47, Appli Sequence 47, Appli Sequence 27, Appli Sequence 36, Appli Sequence 36, Appli Sequence 36, Appli Sequence 37, Appli Sequence 37, Appli Sequence 38, Appli Sequence 37, Appli Sequence 38, Appli Sequence 39, Appli Sequence 39, Appli Sequence 21, Appli Sequence 23, Appli Sequence 24, Appli Sequence 24, Appli Sequence 27, Appli
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RESULT 1 US-09-500-123-12 Sequence 12, A Patent No. 645 GENERAL INFORM APPLICANT: BU APPLICANT: BU APPLICANT: GI APPLICANT: GI TITLE OF INVE TITLE OF INVE TITLE OF INVE GURRENT APPLI CURRENT APPLI CURRENT FILLN		45	44	43	42	41	40	ب ور	ب د د د	36	35	34	33	32	31	30	29	28	
SULT 1  -09-500-123-12  -09-500-123-12  Sequence 12, Application US/09500123  PACENT NO. 6455278  GENERAL INFORMATION:  APPLICANT: Dubin, Adrienne E  APPLICANT: Erlander, Mark G  APPLICANT: Erlander, Mark G  APPLICANT: Glass, Charles A  TITLE OF INVENTION: DNA encoding Is  TITLE OF INVENTION: VR3  TITLE REFERENCE: Human VR3 receptors  CURRENT APPLICATION NUMBER: US/09-05  CURRENT FILING DATE: 2000-02-08		137	137	137	146	146	155	169	169	172	172	172	172	180	210	221.5	227	227	
3-12 (2, Application Ude 6455278 (FORMATION: 1: Dubin, Adrienne 1: Huvar, Arne 1: Glass, Charles 1: Glass, Charles 1: INVENTION: DNA es 1NVENTION: VR3 1PPLICATION UMBER 1PPLICATION UMBER 1PLICATION UMBER 1PLICATION UMBER 1PLICATION UMBER 1 2000-0		3.6	٠					4 4		•	4.5		•	4.7	5.4	5.7	5.9	٠	
Cation US/09500  N: Adrienne E Arne er, Mark G Charles A N: DNA encoding N: VR3 N: VR3 N: DNA recept ON NUMBER: US/0 DIE: 2000-02-08		316	316	316	57	57	1503	1095	1095	1095	1095	1095	1095	1704	1619	1709	71	71	
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oforms of the human	ALIGNMENTS	US-10-115-123-378	US-10-012-542-378	US-09-461-325-378	US-09-978-303-15	-09-235-451-	US-09-600-087-2	IIS-09-679-426-780	US-09-636-215-780	US-09-679-426-778	US-09-685-166A-778	US-09-636-215-778	US-09-112-096-15	US-09-392-812A-2	US-09-392-812A-4	US-09-392-812A-6	US-09-978-303-14	US-09-235-451-14	
Vanilloid Receptor		378,		378	15	Sequence 15. Appl		700	780,	778,	778,	778	15	Ν.	Α.	6	14,	Sequence 14, Appl	

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Db	β	Matches	Query Match	US-09-500-123-12	; ORGANIS	; TYPE: PRT	; LENGTH: 742	; SEQ ID NO 12	; SOFTWARI	; NUMBER (	; CURRENT
1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSDADASRPAGD 60	1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60	Matches 742; Conservative 0; Mismatches 0; Indels 0; Gaps	Query Match 100.0%; Score 3858; DB 4; Length 742; Best Local Similarity 100.0%. Dred No. 0.	-123-12	ORGANISM: Homo sapiens	PRT	H: 742	NO 12	SOFTWARE: PatentIn Ver. 2.1	NUMBER OF SEQ ID NOS: 17	CURRENT FILING DATE: 2000-02-08
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ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI

TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT

240 240

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TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT

KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL

KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL

GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN

GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN

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Sequence 7. Application US/09500123
; Sequence 7. Application US/09500123
; Patent No. 6455278
; Patent No. 10 Maria Carlone E
; Applicant: Huvar, Arne
; Applicant: Erlander, Mark G
; Applicant: Erlander, Mark G
; Applicant: Class, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; TITLE OF INVENTION: VA3 receptors
; CURRENT APPLICATION NUMBER: US/09/500,123
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
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; ORGANISM: Homo sapiens
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Local Similarity 99.9%;
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                                                TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT
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US-09-500-123-9
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CURRENT APPLICATION NUMBER: US/09/500,123
CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 811
TYPE: PRT
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Patent No. 6455278
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Best Local Similarity
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APPLICANT: Huvar, Arne
APPLICANT: Erlander, Mark G
APPLICANT: Glass, Charles A
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                                                                                                           <u>MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP</u>
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                                                     GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN
                                                                                                                                                              89.9%;
ilarity 91.7%;
Conservative
                                                                                                                                                               ; Score 3470; DB; Pred. No. 0; O; Mismatches
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                                                                                       ; TYPE: PRT
; ORGANISM: chicken
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                                           Query Match
Best Local Similarity
Matches 343; Conser
                                                                                                                        SOFTWARE: FastSEQ for Windows Version SEQ ID NO 25
LENGTH: 843
                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/09235451 GENERAL INFORMATION:
                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/235,451
CURRENT FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                              APPLICANT: Julius, David J.
APPLICANT: Caterina, Michael J.
APPLICANT: Brake, Anthony J.
APPLICANT: Brake, Anthony J.
TITLE OF INVENTION: NUCLERIC ACID SEQUENCES ENCODING
TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 9076/004CIP
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     DGEDSAL--ETAD
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                                              Conservative
                                                       41.6%;
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                                            Score 1604.5;
Pred. No. 1.2e-
28; Mismatches
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     -NLOGIF
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L.2e-143;
hes 184;
  ----SNKVQPSKSNIFARRGRFVMG
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KLTIGMGDLEMLSSTKYPVVFIILLTYIILTFVLLLNMLIALMGETVGQVSKESKHIWK 734
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                                                                                              VFLLGFSTAVVTLIED-
                                                                                                                   SVVLYFCGQELYVASMVFSLALGWANMLYYTRGFQQMGIYSVMIAKMILRDLCRFMFVYL
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RESULT 5
US-09-978-303-25
Sequence 25, Application US/09978303
Patent No. 6790629
PATENT INFORMATION:
APPLICANT: Julius, David J.
APPLICANT: Caterina, Michael J.
APPLICANT: Brake, Anthony J.
TITLE OF INVENTION: Nucleic acid sequences encoding
TITLE OF INVENTION: Polypeptides and uses thereof
FILE REFERENCE: UCALO84CON
CURRENT APPLICATION NUMBER: US/09/978,303
CURRENT APPLICATION NUMBER: 09/235,451
PRIOR PILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 09/235,451
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 09/235,451
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0

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; LENGTH: 843
; TYPE: PRT
; ORGANISM: chicken
US-09-978-303-25
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Sequence 2, Application US/09235451

Sequence 2, Application US/09235451

GENERAL INFORMATION:

APPLICANT: Julius, David J.

APPLICANT: Brake, Anthony J.

APPLICANT: Brake, Anthony J.

APPLICANT: Brake, Anthony J.

TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
TITLE OF INVENTION: POLYPEPTIDES AND CAPSAICIN RECEPTOR-RELATED
TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 9076/084CIP
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Best Local Similarity
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FAYILREIKDPECRHLSRKFTEWAYGPVHSSLYDLSCIDTC-EKNSVLEIIAYSSETPN
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RESULT 7 US-09-132-316-3

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CURRENT APPLICATION NUMBER: US/09/235,451
CURRENT FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 838
TYPE: PRT
ORGANISM: R. rattus
US-09-235-451-2
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                                                  NSLPMESTPHKCRGSACKPGNSYNSLYST-CLELFKFTIGMGDLEFTENYDFKAVFIILL
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APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Vanilloid Receptor-2

FILE REFERENCE: 1488,111000

CURRENT APPLICATION NUMBER: US/09/132,316B

CURRENT FILING DATE: 1998-08-11

EARLIER APPLICATION NUMBER: US 60/040,163

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: PCT/US98/04493

EARLIER FILING DATE: 1998-03-06
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Best Local Similarity
Matches 338; Conserv
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SOFTWARE: Patentin Ver. 2.0
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                          CTVP---TYPSCRDS-----ETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILL
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                                                          YTRGFQQMGIYAVMIEKMILRDLCRFMFVYLVFLFGFSTAVVTLI--
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AUTHORS: Caterina, Michael J.
AUTHORS: Schumacher, Mark A.
AUTHORS: Tominage, Makoto
AUTHORS: Tominage, Makoto
AUTHORS: Rosen, Tobias A.
TITLE: The capsaicin receptor: a
TITLE: the pain pathway
YOLUME: 389
PAGERC: OCC.
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US-09-667-422-9
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Best Local S
Matches 338
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: HCR
CURRENT APPLICATION NUMBER: US/09/667,422
CURRENT FILING DATE: 2001-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cortright, Daniel
APPLICANT: Krause, James
TITLE OF INVENTION: Human Capsaicin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGES: 816-824
DATE: 1997
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INVVSYLCAMVIFTLTAYYQPLEGTPPYPYRTTV-DYLRLAGEVITLFTGVLFFFTNIKD
                                                            VYSSLYDLSSLDTCGEEASVLEILVY-NSKIENRHEMLAVEPINELLRDKWRKFGAVSFY
                                                                                                                  ARLFPDSNLEAVLANDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGP
                                                                                                                                                         CTNOLATVKFLLQNSWQPADISARDSVGNTVLHALVEVADNTVDNTKFVTSMYNBILILG
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LAYVILTYILLLNMLIALMGETVNKIAQESKNIWKLQ
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                                           VHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHDMLLVEPLNRLLQDKWDRFVKRIFY
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Pred. No. 3e-141;
9; Mismatches 19
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US-09-978-303-2
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CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/235,451
PRIOR FILLMG DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
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Best Local Similarity
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APPLICANT: Brake, Anthony J.
TITLE OF INVENTION: Nucleic acid sequences encoding
TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
TITLE OF INVENTION: polypeptides and uses thereof
FILE REFERENCE: UCALO84CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Julius, David J.
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CTNOPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKC
                                                                                    IYYRGQTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAA 293
                                                                                                                          ORSKKRLTDSEFKDPETGKTCLLKAMLNLHNGQNDTIALLLDVARKTDSLKOFVNASYTD
                                                                                                                                          LTHKKRLTDEEFREBSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRD 233
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                                                     SYYKGQTALHIAIERRNMTLVTLLVENGADVQAAANGDFFKKTKGRPGFYFGELPLSLAA
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44.6%; Pred. No. 3e-141;
tive 129; Mismatches 193; Indels
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                                                                                                                            APPLICATION NUMBER: UK 9805137.8
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 21-JUL-1998
APPLICATION NUMBER: UK 9819278.4
FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19482-0980
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MEADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 8
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                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. DO. CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                          NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                         FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Ratner & Prestia
            TELEPHONE: 601-407-0701
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DAVIS, JOHN
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RESULT 11
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           Sequence 8, Application US/09197636
Patent No. 6239267
GEMERAL INFORMATION:
APPLICANT: DUCKWORTH, DAVID
APPLICANT: HAYES, PHILIP
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Best Local S
Matches 321
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hes 321;
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STRANDEDNESS: single
TOPOLOGY: linear
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Similarity 44.5%;
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Pred. No. 3.7e-139;
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Best Local S
Matches 321
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APPLICATION NUMBER: UK 981
FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestla, Paul F
REGISTRATION UMBER: 23,03
REFERENCE/DOCKET NUMBER: G
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APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL C
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION NUMBER: UK 9805137.8
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CTTY: Valley Forge
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FILING DATE: 12-MAR-1998
APPLICATION TO THE TOTAL OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 23-NOV-1998
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                                                                      AIADNTRENTKFVTKMYDLLLLKCARLFPDSNLBAVLNNDGLSPLMMAAKTGKIGIFQHI 389
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IRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVY-NSKIENRHE
                                       EVADNTADNTKFVTSMYNEILIIGAKLHPTLKLEELTNKKGMTPLALAAGTGKIGVLAYI
                                                                                                                                                           GRFFQPKDEGGYFYFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALV
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                                                                                                                                 GDFFKKTKGRPGFYFGELPLSLAACTNQLGIVKFLLQNSWQTADISARDSVGNTVLHALV
                                                                                                                                                                                                                        TPILLETARQTDSLKELVNASYTDSYYKGQTALHTATERRNMALVTLLVENGADVQAAAH
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O. Box 980
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Indels Length 839;

74;

Gaps

81 95 12;

-LSQDSVAASTEKTLRLY

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Sequence 34, Application US/09235451

Sequence 34, Application

APPLICANT: Julius, David J.

APPLICANT: Caterina, Michael J.

APPLICANT: Brake, Anthony J.

ITILE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING

ITILE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED

ITILE OF INVENTION: POLYPEPTIDES AND USES THEREOF

FILE REFERENCE: 9076/084CIP

CURRENT APPLICATION NUMBER: US/09/235,451

CURRENT APPLICATION NUMBER: 60/072,151

PRIOR APPLICATION NUMBER: 60/072,151

PRIOR APPLICATION NUMBER: 08/915,461

PRIOR APPLICATION NUMBER: 08/915,461

PRIOR APPLICATION NUMBER: 08/915,461

PRIOR APPLICATION NUMBER: 08/915,461

PRIOR FILING DATE: 1997-08-20

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 34

LENGTH: 839

TYPE: PRIOR

ORGANISM: Homo sapiens

US-09-235-451-34
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                                                                                                                                                                                                        PDPLDGDPNSRPPPAKPOLSTAKSRTRLFGKGDSEEAFPVDCPHEEGELDSCPTITVSPV 81
                                                                                                                                                                                                                                        PSPADASRPAGPGDGRPNL-----RMKFQG-----AFRKGVPNPIDLLES--TLYESSV 95
                   IPVLLDIAERTGNMREFINSPFRDIYYRGQTALHIAIERRCKHYVELLVAQGADVHAQAR 269
Conservative 138; Mismatches 188;
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                                                                                                                                                                                                                                                                                              Score 1556.5; DB 3; Pred. No. 4.7e-139;
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                                                                                                                                                                                                                                                                                                                  Length 839;
                                                                                                                                          --LSQDSVAASTEKTLRLY 113
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CURRENT APPLICATION NUMBER: US/09/978,303
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/235,451
PRIOR FILING DATE: 1999-01-22
PRIOR FILING DATE: 1999-01-22
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FABLEEQ for Windows Version 4.0
SEQ ID NO 34
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US-09-978-303-34
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APPLICANT: Julius, David J.
APPLICANT: Julius, Michael J.
APPLICANT: Erake, Anthony J.
APPLICANT: Brake, Anthony J.
APPLICANTION: Cappsaicin receptor and capsaicin receptor-related TITLE OF INVENTION: polypeptides and uses thereof
FILE REFERENCE: UCAL084COM

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                                                                                                                           Matches
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                               Local Similarity
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                                                       PSPADASRPAGPGDGRPNL----RMKFQG-----AFRKGVPNPIDLLES--TLYESSV 95
PDPLDGDPNSRPPPAKPQLSTAKSRTRLFGKGDSEEAFPVDCPHEEGELDSCPTITVSPV
                                                                                                                           40.3%; Score 1556.5; DB 4; Length 839;
44.5%; Pred. No. 4.7e-139;
Live 138; Mismatches 188; Indels 74;
                                                                                                                                        74;
                                                                                                                                        Gaps
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APPLICANT: Mcintyre, Peter
APPLICANT: James, Iain Fraser
TITLE OF INVENTION: Human Vanilloid Receptor
FILE REFERENCE: 4-30875A
CURRENT APPLICATION NUMBER: US/09/533,220A
CURRENT FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: UNITED KINGDOM 990705
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 1.30
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                                                                                            SEQ ID NO 2
LENGTH: 839
                                                                                                                                                                                                                                                   Sequence 2, Application US/09533220A Patent No. 6406908 GENERAL INFORMATION:
      Best Local Sin
Matches 321;
                                Query Match
                                                        TYPE: PRT
ORGANISM: Homo
:-09-533-220A-2
                 Local Similarity
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    40.3%; Score 1555.5; DB 4;
44.5%; Pred. No. 5.8e-139;
tive 137; Mismatches 189;
                                                                                                                                                            KINGDOM 9907097.1
     Indels
                            Length 839;
     74;
     Gaps
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                                                                                                Sequence 4, Application US/09197
Patent No. 6239267
; GENERAL INFORMATION:
APPLICANT: DUCKWORTH, DAVID
APPLICANT: HAYES, PHILIP
APPLICANT: MEADOWS, HELEN
APPLICANT: MEADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: MOVEL CO
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US-09-197-636-4
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & P.
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: US
ZIP: 19482-0980
COMPUTER READABLE FORM:
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                                                                                                                                                    DUCKWORTH, DAVID HAYES, PHILIP
                                                                            & Prestia
                                                                                                                 COMPOUNDS
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293 329 269 173 113 149 81 95

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-197-636-4
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9805137.8
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 21-JUL-1998
APPLICATION UNMBER: UK 9819278.4
FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 846169
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,636
FILLING DATE: 23-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 601-407-0700
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COMPUTER: IE
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REFERENCE/DOCKET NUMBER: GP-30075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Prestia, Paul F
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
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                                                                                                                              270 GRFFQPKDEGGYFYFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALV 329
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                                                                                   509 LRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFIDGSFQLLYFIYSVLVIVSAALYL 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 PDPLDGDPNSRPPPAKPQLSTAKSRTRLFGKGDSEEAFPVDCPHEEGELDSCPTITVSPV
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                                                                                                                                                                                                                                                                                                                                                                                             NRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITIQRPGDGPTGARL-----
                                          IPLLLEIARQTDSLKELVNAXYTDXYYKGQTALHIAIERRNMALVTLLVENGADVQAAAH 233
AGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLERFLLVYLLFMIGY 628
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Search completed: December 2, 2004, 22:36:13 Job time : 45 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                 US-10-090-215-12
3858
1 MADSSEGPRAGPGEVAELPG......GQVSKESKHIWKLQSGRRRL 742
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/cgn2_6/ptodata/1/pubpaa/US08 NEW PUB-COMB.pep: *
/cgn2_6/ptodata/1/pubpaa/US08 NEW PUB-COMB.pep: *
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/cgn2_6/ptodata/1/pubpaa/US09A PUBCOMB.pep: *
/cgn2_6/ptodata/1/pubpaa/US09A PUBCOMB.pep: *
/cgn2_6/ptodata/1/pubpaa/US09B PUBCOMB.pep: *
/cgn2_6/ptodata/1/pubpaa/US09C PUBCOMB.pep: *
/cgn2_6/ptodata/1/pubpaa/US09C PUBCOMB.pep: *
/cgn2_6/ptodata/1/pubpaa/US10A PUBCOMB.pep: *
/cgn2_6/ptodata/1/pubpaa/US10B PUBCOMB.pep: *
/cgn2_6/ptodata/1/pubpaa/US10B PUBCOMB.pep: *
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/cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep: *
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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<b>5</b>	7,	N	10	Sequence 4. Appli	Sequence 4. Appli	Sequence 1506, Ap	Sequence 1507, Ap	equence	Sequence 11, Appl	Sequence 36, Appl	5. App	e .	œ.	N			_		۳.	14.	φ.		10	Sequence 80. Appl	9 1	D 1	ים פיים	equence 84	e 3. Anr	e 1477.	P S

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; Sequence 12, Application US/10090215
; Publication No. US20030032097A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     US-10-090-215-12
                                                                                                                                                                                                                                                                                                                                                                           PILE REFERENCE: Human VR3 receptors
CURRENT APPLICATION NUMBER: US/10/090,215
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 17
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 742
                                                                                                                                                                                                                            Query Match 100.0%; Score 3858; DB 14; Best Local Similarity 100.0%; Pred. No. 1.7e-307; Matches 742; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dubin, Adrienne E
APPLICANT: Huvar, Arne
APPLICANT: Erlander, Mark G
APPLICANT: Glass, Charles A
TITLE OF INVENTION: DNA encoding Isoforms
TITLE OF INVENTION: VR3
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL
                                                                        61
                                                                                     61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
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APPLICANT: ROOS, Jack
APPLICANT: Stauderman, Kenneth
APPLICANT: Velicelebi, G"n_1
APPLICANT: Velicelebi, G"n_1
TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
TITLE OF INVENTION: METHODS: US/10/342,844
CURRENT APPLICATION NUMBER: US/10/342,844
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US 60/347,459
PRIOR APPLICATION NUMBER: US 60/401,171
PRIOR FILING DATE: 2002-08-02
PRIOR FILING DATE: 2002-08-02
PRIOR FILING DATE: 2002-08-02
PRIOR FILING DATE: 2002-08-02
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 115
SECTIMARE: FastSEQ for Windows Version 4.0
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                                                        SEQ ID NO 76
LENGTH: 831
TYPE: PRT
ORGANISM: Homo 8
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                              Sequence 76, Application US/10342844 Publication No. US20040009537A1 GENERAL INFORMATION:
NAME/KEY: VARIANT
LOCATION: 804, 816
OTHER INFORMATION: Xaa = Any
PUBLICATION INFORMATION:
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    Sequence 2, Application US/10761065

Publication No. US20040137573A1

GENERAL INFORMATION:

APPLICANT: Fizer, Inc.

APPLICANT: Katsuhiro Shinjo

APPLICANT: Hikaru Yabuuchi

TITLE OF INVENTION: Human Vanilloid Receptor-Like Pro

FILE REFERRICE: PC9979ADAM

CURRENT APPLICATION NUMBER: US/10/761,065

CURRENT FILING DATE: 2004-01-20
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RESULT 3 US-10-761-065-2

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Best Local Similarity
Matches 736; Conserv
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                                                          RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE
                                                                                                                                      TVGQVSKESKHIWKLQ 736
                                             RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE
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TVGQVSKESKHIWKLQ 736
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Pred. No. 5e-305;
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Matches 736
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LENGTH: 870
TYPE: PRT
ORGANISM: Human
S-10-761-065-2
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: US 60/208,156
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
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Application US/09870090 No. US20030017527A1
                                                         TVGQVSKESKHIWKLQ
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100.0%; Pred. No. 5.3e-305;
Live 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Pfizer Product Inc.
TITLE OF INVENTION: Human Vanilloid Receptor
FILE REFERENCE: PC9979A
CURRENT APPLICATION NUMBER: US/09/870,090
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: US/09/870,090
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 871
TYPE: PRT
ORGANISM: Human
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           RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE
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Pred. No. 5.3e-305;
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Publication No. US20030027164A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING A 1
TITLE OF INVENTION: HUMAN ION CHANNEL EXPRESED IN SPINAL CORD AND BRAIN
FILE REFERENCE: D0109NP
CURRENT APPLICATION NUMBER: US/10/000,823
CURRENT APPLICATION NUMBER: 60/250,587
PRIOR APPLICATION NUMBER: 60/250,587
PRIOR APPLICATION NUMBER: 60/250,587
PRIOR PILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
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TYPE: PRT
ORGANISM: Homo sapiens
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              RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE
                                                                                           TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC
                                                                      TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC
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PRIOR FILLING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/357,161
PRIOR APPLICATION NUMBER: 60/357,161
PRIOR APPLICATION NUMBER: 60/357,161
PRIOR FILLING DATE: 2002-02-2
PRIOR FILLING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: 60/357,161
PRIOR FILLING DATE: 2002-05-15
PRIOR FILLING DATE: 2002-05-15
PRIOR FILLING DATE: 2002-05-16
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US-10-171-319-17
; Sequence 17, Applicat
; Publication No. US200
; Publication INFORMATION:
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; ORGANISM: Homo
US-10-171-319-17
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 17
LENGTH: 871
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                       NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD
                                                                                ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
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    NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD
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APPLICANT: Roos, Jack
APPLICANT: Stauderman, Kenneth
APPLICANT: Velicelebi, G"n_1
APPLICANT: Velicelebi, G"n_1
TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
FILE REFERENCE: 37481-3307
CURRENT APPLICATION NUMBER: US/10/342,844
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US 60/347,459
PRIOR FILING DATE: 2002-08-02
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-342-844-54
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Matches 736
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LENGTH: 871
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Publication No. US20040009537A1
GENERAL INFORMATION:
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank XP_027181
DATABASE ENTRY DATE: 2002-09-01
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                                                      KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL
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APPLICANT: Scauderman, Kenneth
APPLICANT: Scauderman, Kenneth
APPLICANT: Velicelebi, G"n_1
ITILE OF INVENTION: METHODS OF MODULATING ANI
ITILE OF INVENTION: METHODS OF MODULATE INT
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ITILE OF INVENTION: METHODS OF MODULATE INT
ITILE OF INVENTION: AGENTS THAT MODULATE INT
CURRENT APPLICATION NUMBER: US/10/342,844
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US 60/41,171
PRIOR FILING DATE: 2002-08-02
PRIOR FILING DATE: 2002-08-02
PRIOR FILING DATE: 2002-08-20
AUMBER OF SEQ ID MOS: 115
SOFTWARR: FASTSEQ for Windows Version 4.0
SEQ ID MO 58
LENGTH: 871
                                                                                       US-10-342-844-58
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US-10-342-844-58
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                Query Match
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Matches 736;
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                                                                                                    ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank BAB69040
DATABASE ENTRY DATE: 2001-10-02
                                                                                                                                                                            TYPE: PRT
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                  ilarity 100.0%; | Conservative 0;
                                99.2%; Score 3829; DB 15; 100.0%; Pred. No. 5.3e-305;
              Mismatches
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CURRENT APPLICATION NUMBER: US/10/342,844
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US 60/347,459
PRIOR FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/401,171
PRIOR APPLICATION NUMBER: US 60/405,678
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/405,678
PRIOR FILING DATE: 2002-08-20
NUMBER OF SEQ ID NOS: 115
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Publication No. US20040009537A1
GENERAL INFORMATION:
APPLICANT: Roos, Jack
APPLICANT: Stauderman, Kenneth
APPLICANT: Velicelebi, G"n_1
                                                                                                                                     APPLICANT: Stauderman, Kenneth
APPLICANT: Velicelebi, G'n I
TITLE OF INVENTION: METHODS OF MODULATING
TITLE OF INVENTION: AGENTS THAT MODULATE
FILE REFERENCE: 37481-3307
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RESULT 10 US-10-415-570A-2

Sequence 2, Application US/10415570A Publication No. US20040198649A1 GENERAL INFORMATION: APPLICANT: Davis, John Beresford

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; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 78
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAGI
; DATABASE ENTRY DATE: 2000-09-26
US-10-342-844-78
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Pred. No. 5.3e-305;
D; Mismatches 0;
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Best Local S
Matches 736
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LENGTH: 871
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ORGANISM: Homo
-10-415-570A-2
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version
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FILE REFERENCE: P32689
CURRENT APPLICATION NUMBER: US/10/415,570A
CURRENT FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: PCT/GB01/04739
PRIOR FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: GB 0026114.9
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Egerton, Julie
Smart, Darren
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; TYPE: PRT
; ORGANISM: Homo s
US-10-027-828-2
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Publication No. US20030013650A1
GENERAL INFORMATION:
APPLICANT: Heller, Wolfgang
APPLICANT: Hudspeth, Albert J.
APPLICANT: Friedman, Jeffrey M.
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Best Local Similarity
Matches 735; Conserv
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
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APPLICANT: Friedman, Jeffrey M.
APPLICANT: Friedman, Jeffrey M.
TITLE OF INVENTION: VR-OAC, AN USES THEREOF
FILE OF INVENTION: IT, AND USES THEREOF
FILE REFERENCE: 600-1-287N
CURRENT FAPPLICATION NUMBER: US/10/027,828
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 60/243,568
PRIOR APPLICATION NUMBER: US 60/243,568
PRIOR FILING DATE: 2000-10-26
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TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC
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                                                     NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG
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Pred. No. 6.4e-305;
1; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/342,844
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US 60/347,459
PRIOR FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/401,171
PRIOR APPLICATION NUMBER: US 60/405,678
PRIOR APPLICATION NUMBER: US 60/405,678
PRIOR FILING DATE: 2002-08-02
PRIOR FILING DATE: 2002-08-20
NUMBER OF SEQ ID NOS: 115
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Publication No. US20040009537A1

GENERAL INFORMATION:
APPLICANT: Roos, Jack
APPLICANT: Stauderman, Kenneth
APPLICANT: Velicelebi, G"n_1

TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 60 LENGTH: 871
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AAG28029
DATABASE ENTRY DATE: 2000-10-31
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                      NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
                                                                                    VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLLKCARLFPDS
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NLEAVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFXDWAYGFVYSSLYD
                                                                                                                                                              ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
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                                                                 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS
                                                                                                                               KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL
                                                                                                                                                                                                 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVILDIAERTGNMRBFINSPFRDIYYRGQT
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Pred. No. 6.4e-305;
1; Mismatches 0;
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publication No. US20030013650A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liedtke, Wolfgang
APPLICANT: Heller, Stefan
APPLICANT: Hudspeth, Albert J.
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US-10-027-828-4
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Best Local Similarity 99.9%;
Matches 735; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 4
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APPLICANT: Friedman, Jeffrey M.
TITLE OF INVENTION: VR-OAC, AND USES THEREOF
FILE REFERENCE: 600-1-287N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/027,828
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 60/243,568
PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
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                   ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
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                                                                                    TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT
                                                                                                                                     KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL
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Pred. No. 1.1e-304;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                     Length 871;
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APPLICANT: Dubin, Adrienne E
APPLICANT: Huvar, Arne
APPLICANT: Huvar, Arne
APPLICANT: Briander, Mark G
APPLICANT: Briander, Mark G
APPLICANT: Glass, Charles A
TITLE OF INVENTION: DNA encoding Isoforms of
TITLE OF INVENTION: VR3
FILE REFERENCE: Human VR3 receptors
CURRENT APPLICATION NUMBER: US/10/090,215
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 871
TYPE: PRT
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Matches 735
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Publication No. US20030032097A1
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                                                                                                                                                                                                                                            Score 3823; DB 14;
Pred. No. 1.7e-304;
0; Mismatches 1;
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                             ; LENGTH: 963
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Descripti
; OTHER INFORMATION: nucleotid
US-09-932-165-1477
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                                                                                                                                         PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1477
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   Query Match
                                                                                                                                                                                                                  APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITS, AYA
APPLICANT: JAKOBOVITS, AYA
ITITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 83P2H3 AND CATLF2E11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
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LEVIN, ELANA
HUBERT, RENE
GE, WANGMAO
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FARIS, MARY
SAFFRAN, DOUGL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLEAVLANDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNYLTENPHKKADMERODSEGNITVLHALVAIADNITENTKEVIKMYDLLLLKCARLEPDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
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                                              Description of Unknown Organism: CaTrF2E11 nucleotide sequence
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   98.8%;
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   Score
   3810;
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720 660 660

720

540 540 480 480

	TVGQVSKESKHIWKIQ 828	813	дb
	TVGQVSKESKHIWKLQ 736	721	φ
812	RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTXIILTSVLLLNMLIALMGE	753	라
720	RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLTALMGE	661	ફ
752	TYSIMIQKILEKULFRELLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC	693	멍
660	TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC	601	Ş
692	NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAMMVFALVLGWMNALYFTRGLKLTG	633	망
600	NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIBAYLAVMVFALVLGMWAXYFTRGLKXLTG	541	8
632	AMVIFILIAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV	573	망
540	AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV	481	νQ
572	LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC	513	DЪ
480	LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC	421	ર્જ
512	NLEAVLANDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKSKDWAYGPVYSSLYD	453	D
420	NLEAVLNNDGLSPLAMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD	361	Ş
452	VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS	393	뫄
360	vs	301	Qy
392	ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI	333	뮍
300		241	8
332		273	Ъ
240	TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNWREFINSPFRDIYYRGQT	181	Ş
272		213	ф
180	KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPELLTHKKKL	121	Ş
212		153	Дb
120	GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN	61	Ş
152	ъ-	93	g
60	MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP	1	Ş
0;	Local Similarity 99.6%; Pred. No. 2.3e-303; es 733; Conservative 1; Mismatches 2; Indels 0; Gaps	Best Local & Matches 73	X B

Search completed: December 2, 2004, 22:39:18 Job time : 152 secs

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Copyright GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd

3 protein protein search, using sw model

December 2 2004, 22:17:36; Search time 44 Seconds
(without alignments)
1622.565 Million cell updates/sec

Title: Perfect score:

US-10-090-215-12 3858 1 MADSSEGPRAGPGEVAELPG... GQVSKESKHIWKLQSGRRRL

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB Maximum DB веq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

4:2: pir1:\*
pir2:\*
pir3:\*
pir4:\*

Database

PIR 79:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Result No.	Score	Query Match I	Length	DВ	Ħ	Description
י בי בי	. ,	40.9	838	ָם מ	T09054	capsaicin receptor
2	1551.5	40.2	839	N	JC7621	н,
ω	•	19.1	727	N	JC7796	$\mathbf{r}$
4,	724.5	18.8	725	N	JC7531	ra
տ	719	18.6	723	N	JC7795	עם
o,	473.5		937	N	T37241	a
7	473.5		957	N	D88651	tein B0212.5
8	435.5	11.3	900	N	T33026	8
9	313.5		790	N	T20312	
10	278		519	N	T24772	_
11	204.5	5.3	1188	N	T19552	
12	188		828	N	JC5807	Þ
13	145.5		1124	N	JH0588	calmodulin-binding
14	138.5		810	N	I38361	TRPC1 protein - hu
15	137	3.6	616	N	T00894	hypothetical prote
16	w		1765	N	T42388	
17	136.5		683	N	A85044	
18	136	٠	2352	N	T30201	ഥ
19	134	٠	1275	N	JU0092	trp protein - frui
20	133	٠	481	N	T23729	r r
21	132		1274	N	JN0015	
22	٠		642	N	S58154	othetical p
23	•		652	N	D85044	
24	129.5		809	N	G02640	ζ.
25	129		823	N	S44873	prot
26	127.5		4377	N	ASS575	long s
27	126.5		643	N	D86167	F21B7.27
28	126.5	ω ω	2471	N	A49128	~
29	126		2212	N	A41098	

44	4 2	40 41	9 8 9	37	ر بر	ω μ 4 μ	32	31	30
119 119	120 119.5	120.5	121 120.5	121	123	123.5	125	125.5	125.5
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T42714 T42715	T27499	D86464	T13940 T46445	JC7995	F85043	S68238 A37867	S68453	B64635	H71274
ankyrin 3, splice ankyrin 3, splice	hypothetical prote	מל ל	ankyrin - fruit fl hypothetical prote	transient receptor	hypothetical prote	trp-1 protein - hu transcription fact	sodium channel pro	toxin-like outer m	probable ankyrin -

#### ALIGNMENTS

A;Cross-references: UNIPROT:035433; EMBL:AF029310; NID:g2570932; PIDN:AAC53398.1; PID:gA;Experimental source: dorsal root ganglion C;Keywords: ion channel; receptor A;Title: The capsaicin receptor: A heat-activated ion channel A;Reference number: Z16539; MUID:98007969; PMID:9349813 A;Accession: T09054 capsaicin receptor - rat
N;Alternate names: vanilloid receptor subtype 1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004
C;Accession: T09054 R;Caterina, M.J.; Schumacl Nature 389, 816-824, 1997 A; Molecule type: mRNA A; Residues: 1-838 < CAT> A; Status: preliminary; translated from GB/EMBL/DDBJ Query Match
Best Local Similarity Schumacher, M.A.; Tominaga, M.; Rosen, T.A.; Levine, J.D.; Julius, 40.9%; Score 1579.5; DB 2; Pred. No. 1.1e-103; 9; Mismatches 193; Length in the pain pathway. 838;

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В S 밁 ঠ Ś 밁 S 밁 Ş 뮹 Ş 밁 Ş 뭥 Matches 414 317 257 294 197 234 IYYRGQTALHIAIERRCKHYVELLVAQQADVHAQARGRFFQPKDEGGYFYFGELPLSLAA 293 137 354 174 LTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRD 233 114 RHHSSDNKRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFL 338; 95 64 55 16 ហ VYSSLYDLSSLDTCGEEASVLEILVY-NSKIENRHEMLAVEPINELLRDKWRKFGAVSFY ARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGP 413 CTNOPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKC 353 PYEEG----AKLHPTLKLEEITNRKGLTPLALAASSGKIGVLAYILQREIHEPECRHLSRKFTEWAYGP CINQLAIVKFLLQNSWQPADISARDSVGNTVLHALVEVADNTVDNTKFVTSMYNEILILG SYYKGOTALHIAIERRNMTLVTLLVENGADVQAAANGDFFKKTKGRPGFYFGELPLSLAA QRSKKRITDSEFKDPETGKTCLLKAMLNIHNGQNDTTALLLDVARKTDSLKQFVNASYTD RPSSQDS----SRPAGPGDGRENLRMKFQGAFRKGVPN-PIDLLESTLYESSVVPGPKKAPMDSLEDYGTY 113 ASIDSEESESPPQENSCIDPPDRDPNCKPPPVKPHIFTTRSRTRLF-GKGDSEEASPLDC AELPGDESGTPGGE---------AFPLSSLANLFEGEDGSLSPSPADA 54 Conservative 129; --VSAGEKPP--RLYDRRSIFDAVAQSNCQELESLLPFL --GLASCPITTVSSVI----TIQRPGDGP-----ASV 94 Indels 97; Gaps 173 316 196 136 63 256 16;

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A;Map position: 17p13
C;Keywords: transmembrane protein
F;201-23/Domain: ankyrin #status predicted <ANK1>
F;201-23/Domain: ankyrin #status predicted <ANK2>
F;248-280/Domain: ankyrin #status predicted <ANK2>
F;333-365/Domain: transmembrane #status predicted <TM1>
F;473-495/Domain: transmembrane #status predicted <TM2>
F;477-495/Domain: transmembrane #status predicted <TM3>
F;508-531/Domain: transmembrane #status predicted <TM4>
F;578-597/Domain: transmembrane #status predicted <TM4>
F;578-597/Domain: transmembrane #status predicted <TM5>
F;624-644/Region: pore loop #status predicted <TM6>
F;626-684/Domain: transmembrane #status predicted <TM6>
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A;Residues: 1-839 <COR>
A;Cross-references: UNIPROT:Q9H304; GB:AF196175
C;Comment: This receptor, a transmembrane protein with many phosphorylation sites,
its integrative activation by several noxious stimuli, and plays an important role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Cortright, D.N.; Crandall, M.; Sanchez, J.F.; Zou, T.; Krause, J.E.; White, Biochem. Biophys. Res. Commun. 281, 1183-1189, 2001
A;Title: The tissue distribution and functional characterization of human VR1.
A;Reference number: JC7621; MUID:21139751; PMID:11243859
A;Contents: Dorsal root ganglia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capsaicin receptor, VR1 - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7621
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                                                                                          150 NRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDT
                                                                                                                                                                                 96 V-----PGPKKAPMDSLFDYGTYRHHSSDNKRWRKKIIEKQPQSPKAPAPQPPPILKVF
                                                                                                                                         82 ITIQRPGDGPTGARL---
                                                                                                                                                                                                                                                                              49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFLQRRPSLKSLFVDSYSBILFFVQSLFMLVSVVLYFSQRKEYVASMVFSLAMGWINNLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FNFFVYCLYMIIFTAAAYYRPVEGLPPYKLKNTVGDYFRVTGEILSVSGGVYFFPRGIQ- 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHDMLLVEPLNRLLQDKWDRFVKRIFY
                                               NSLPMESTPHKCRGSACKPGNSYNSLYST-CLELFKFTIGMGDLEFTENYDFKAVFIILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTRGLKLTGTYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTN :||| : | | ::|:|:|:|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTVP---TYPSCRDS-----ETFSTELLDLFKLTIGMGDLEMLSSTKYPVVFIILL
  IPVLLDIAERTGNMREFINSPFRDIYYRGQTALHIAIERRCKHYVELLVAQGADVHAQAR
                                                                                                                                                                                                                                   PDPLDGDPNSRPPPAKPQLSTAKSRTRLFGKGDSEEAFPVDCPHEEGELDSCPTITVSPV
                                                                                                                                                                                                                                                                         PSPADASRPAGPGDGRPNL-----RMKFQG-----AFRKGVPNPIDLLES--TLYESSV
                                                                                                                                                                                                                                                                                                                           Conservative 138;
                                                                                                                                                                                                                                                                                                                                              40.2%;
                                                                                                                                                                                                                                                                                                                                                  Score 1551.5; DB 2
Pred. No. 1.1e-101;
                                                                                                                                                                                                                                                                                                                             Mismatches 189; Indels
                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T.; Krause, J.E.; White,
                                                                                                                                           -----LSQDSVAASTEKTLRLY 113
                                                                                                                                                                                                                                                                                                                                                                        Length 839;
                                                                                                                                                                                                                                                                                                                             74;
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R;Weber, K.; Erben, R.G.; Rump, A.; Adamski, J.
Biochem. Biophys. Res. Commun. 289, 1287-1294, 2001
A;Title: Gene structure and regulation of the murine epithelial calcium channels ECaCl
A;Reference number: JC7795
A;Accession: JC7796
A;Accession: JC7796
A;Molecule type: DNA
A;Residues: 1-727 <WEB>
A;Gross-references: UNIPROT:Q91WD2; GB:AF336378
A;Cross-references: UNIPROT:Q91WD2; GB:AF36378
C;Comment: This calcium channel plays an important role in active transcellular calcium
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                                                                                                                                                                             relevant for in vivo calcium homeostasis.
                                                                                                                                                                                                                                                                                                                                   epithelial calcium channel 2, ECaC2 - mouse
N;Alternate names: calcium T; CaT1
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-2002 #sequence_revision 17-May-2002 #text_change 09-Jul-2004
C;Accession: JC7796
C;Accession: JC7796
R;Weber, K; Erben, R.G.; Rump, A.; Adamski, J.
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                                                                                                                     A;Gene: ECaC2
A;Map position: 6
A;Introns: 43/2; 76/1; 117/1; 163/1; 196/1; 253/3; 302/3; 373/3; 402/3; C;Keywords: calcium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             吊
                                                                          Query Match
Best Local
                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 GRFFQFKDEGGYFYFGELFLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALV
 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVADNTADNTKFVTSMYNEILMLGAKLHPTLKLEELTNKKGMTPLALAAGTGKIGVLAYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STAVVILI ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASALVSLLNPCANMKVCNEDQTNCTVPTY-----PSCRDSET-----FSTFLLDLFK 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHLKEYVASMVFSLALGWTNMLYYTRGFQQMGIYAVMIEKMILRDLCRFMFVYIVFLFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFLLVYLLFMIGY 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFIDGSFQLLYFIYSVLVIVSAALYL
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EEFREPSTGKTCLPKALL--NLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGOT
                                                             Conservative 101;
                                                                           19.1%; Score 736.5; DB 2 33.3%; Pred. No. 4.4e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDGKNDSLESESTSHRWRGPACRPPDSSYNSLYST-CLELFK
                                                                Mismatches 193;
                                                                                           DB 2;
                                                                Indels
                                                                                           Length
                                                                99;
                                                                Gaps
                                                                                                                                            428/2; 483/3;
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                                                                 21;
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241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

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RESULT 4

JC7531

calcium transport protein, CaT1 - human

cispecies: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C;Accession: JC7531

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev

R;Peng, J.B.; Line, Li
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A;Map position: 7q33-34
C;Keywords: calcium channel; calcium transport; intestine; kidney; transmembrane
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A;Molecule type: mRNA
A;Residues: 1-725 <PEN>
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                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
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                                                                                                                                                                                                                                                             PFLLTHK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YIIFQ----TEDEDELGHFYDYPMA----LFSTF--ELF-LTIIDGPANYDVDL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYSSLYDLSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRLLIEH---GADIRAQDSLGNTVLHILI-----LQPNKTFACQMYNLLLSYDGGDHLK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALHIAVINQNVNLVRALLARGASVSARATGSVFHYRPH-NLIYYGEHPLSFAACVGSEEI 178
                                                                           EGGYFYFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STKYPVVFIILLVTYIILTFVLLLNMLIALMGETVGQVSKESKHIWKLQ
                                                                                                                                                                  ERTGNMREFINSPERDIYYRGQTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKD
                                                                                                                                                                                                               PLLLAAKDNDVQALNKLLKYEDCKVHHRGAMGETALHIAALYDNL----EAAMVLMEAA
    NTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDE
                                              PCNLIYFGEHPLSFAACVNSEEIVRLLIEH----GADIRAQDSLGNTVLHILI------LQP
                                                                                                                                                                                                                                                                                                   Conservative
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32.9%;
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A; Introns: 37/2;
C; Keywords: calc
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epithelial calcium channel 1, ECaCl - mouse
(;Species: Mus musculus (house mouse)
(;Species: Mus musculus (house mouse)
C;Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
C;Accession: JC7795
C;Accession: JC7795
R;Weber, K; Erben, R.G.; Rump, A.; Adamski, J.
R;Weber, K; Erben, R.G.; Rump, A.; Adamski, J.
R;Weber, K; Erben, R.G.; Rump, A.; Adamski, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              relevant for in vivo calcium C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 289, 128
A;Title: Gene structure and regulation
A;Reference number: JC7795
A;Accession: JC7795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AF336378
C;Comment: This calcium channel plays an
relevant for in vivo calcium homeostasis.
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                                                                                                                                                                        MREFINSPFRDIYYRGQTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYF
                                                                                                                                                                                                                             MCTLKKLQHDQNCDFRQRGALGETALHVAALYDNL----DAAIMLMEAAPYLVTEST--
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COMYNILLISYDGGDHLK
                                    TKMYDLLL-----
                                                                                                 YFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFV
                                                                                                                                                                                                                                                                                                                                                                                       : 6
2; 70/1; 111/1; '
                                                                       YYGEHPLSFAACVGSEEIVRLLIEH---GADIRAQDSLGNTVLHILV-----LQPNKTFA
                                                                                                                                                                                                                                                                                                          Conservative 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R.G.; Rump, А.;
ев. Commun. 289,
                                                                                                                                                ----VGQTALHIAVMNQNVNLVRALLARGASASARATGSAFH-RSSHNLI
                                                                                                                                                                                                                                                                                                                            18.6%;
                  LKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVT 395
                                                                                                                                                                                                                                                                                                                                                                                                       157/1; 190/1;
                                                                                                                                                                                                                                                                                                          Score 719; DB 2;
Pred. No. 7.6e-43;
00; Mismatches 198
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1287-1294, 2001
ion of the murine
SLELVPNNQGLTPFKLAGVEGNTVMFQHLMQK----
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453 EPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLTAYYQPLEGTPPYPYRTTVDYL 509 Db	397 EDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVXNSKIENRHEMLAV 452	337 ENTKPVTKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTD 396	280 GYFYFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTR 336 Db	233 DIYYRGQTALHIAIERRCKHYYELLVAQGADVHAQARGRFFQDKDEG 279	Overy Match 12.3%; Score 473.5; DB 2; Length 937; Db 26 Db 27 Db 28 Db 27 Db 27 Db 28 Db 28 Db 29 Db 20 Db 2	PRC	Bargmann, C.I. 1997 In with structural similarity to channels, is required for 11D:97477445; PMID:9334401	rotein osm-9 - Caenorhabditis elegans bditis elegans #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004		674 FKLTIGMGDLEMLSSTKYPVVEIILLVTYIILTFVLLLNMLIALMGETVGQVSKESKHIW 733	615 FRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNC-TVPTYPSCRDSETFSTFLLDL 673	555 IYSVLVIVSAALYLAGIEAYLAVMVFALVLGMNNALYFTRGLKLTGTYSIMIQKILFKDL 614 Qy  :   :   :	499 PYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFIDGSFQLLYF 554	456 NELLRDKWRKFGAVSFYINVVSYLCAMVIFTLTAYYQPLEGTP 498   :   : :   :            :   :   :   :	396 DEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPI 455  Qy 256RKRIQWSFGPLTSSLYDLTEIDSWGEELSFLELVVSSKKKEAR-QILEQTPV 306  Db
434 RTACELLTILNCIFFVGYQQLGEIRTQGMR 554 FIYSVLVIVSAALYLAGIEAYLAVMVFALV	376 EVIQELLADKWKAFAQRKLIERLVLLIVQL 510 RLAGBVITLFTGVLF	322IMKVEFWRESDMTCSAYPINTIDT 453 EPINELLEDKWRKFGAVSFYINVSYLCAM	273INYSSSMYSYAVRHWAKPADPHVV 397 EDTRHLSRKFKDWAYGPVYSSLYDLSSLDT	226 GYAYYGEYPLAFAACFGNKDIYDLLIQFGA 337 ENTKFVTKNYDLLLLKCARLFPDSNLEAVL	TATED DEORG PADED	8 0 3	: pre lle ty les: 1 refer conta .cs: B0212	R; annoymous, The C. elegans Sequencing Consc Science 282, 2012-2018, 1998 A;Title: Genome sequence of the nematode C. A;Reference number: A75000; MUID:99069613; F A;Note: see webbites genome.wustl.edu/gsc/C A;Note: published errata appeared in Science A;Notes: 188651	2.5 [im] aenorhal ay-2001 D88651	7	728 BSKHIWKLQ 736 :::  :   651 QAEKAWRQQ 659	668 TFLLDLFKLTIGMGDLEMLSSTKYPVVFII	614 LFRELLVYLLFMIGYASALVSL-LNPCANN       ::     ::   537 MIRFAIISAIFLVSFSQVFYFVGKDMDAK(	554 FIYSVLVIVSAALYLAGIEAYLAVMVFALY	510 RLAGEVITLETGVLE

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TILLUTYIILTFULLLNMLIALMGETUGQUSK 727
                                                             KOKLEDTNPHACRISGYTIYTY-----NTEP 590
                                                                                                                                                                                   : |:|
MRGYLRNLKTAPAKAVFCIANLFL----- 482
                                                                                             NMKVCNEDQTNC----TVPTYPSCRDSETFS 667
                                                                                                                         LVLGWMNALYFTRGLKLTGTYSIMIQKILFKD 613
                                                                                                                                                                                                           ---FFTNIKDLFMKKCPGVNSLFIDGSFQLLY 553
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. elegans: a platform for investigating biolog PMID:9851916
C elegans/ and www sanger.ac.uk/Projects/C ele ce 283, 35, 1999; Science 283, 2103, 1999; and в elegans ortium.

\_IV; PIDN:AAC02569.1; PID:g2854148; GSPDB:GN00eats

MVIFTLTAYYQPLEGTPPYPYRTTV---DYL 509 LVAQGADVHAQARGREFQPK-----DEG 279 3.5; DB 2; Length 957; . 2.7e-25; cches 213; Indels 97; Gaps VLGWMNALYFTRGLKLTGTYSIMIQKILFKD 613 RGYLRNLKTAPAKAVFCIANLFL-----TIQPDGSTNYDSALMTVINGSTPEHLDMIGS 375 \*|: | :|| :| | : ||: ::
VNHAGFTPLTLATKLGRKQIFEEMLE---- 321 "LNNDGLSPLMMAAKTGKIGIFQHIIRREVTD 396 --FFTNIKDLFMKKCPGVNSLFIDGSFQLLY 553 TCGEEASV----LEILVYNSKIENRHEMLAV 452 485

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hypothetical protein T09A12.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change C;Accession: T33026
R;Hawkins, J.; Fulton, B.; Gillam, B.
submitted to the EMBL Data Library, February 1998
submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid T09A12.
A;Steference number: Z21265
A;Accession: T33026
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Introns: 43/2, 86/3; 260/2; 396/3; 424/2; 495/1; 517/3; 553/3; 691/3;
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A;Residues: 1-900 <HAW>
A;Cross-references: UNIPROT:O61220; EMBL:AF047660; PIDN:AAC04431.1;
A;Experimental source: strain Bristol N2; clone T09A12
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                GICVQVFLDERDIKRIGRKKWWNVLTAFPAKITFKLTYFLVLAMIPTRLACDLSPVLLVV
                                                                                                                                                                             BLLRDKWRKFG----AVSFYINVVSYLCAMVIFTL-----
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                                                TLFTGVLFFFTNIKDLFMKKCPGVNSLF-IDGSFQLLYFIYSVLVIVSAALYLAGIEAYL
                                                                                                                                                           TLLEAKWEAFAKRNMIVSFTAFTLYYICFVTAFTLRPIGFSTEMLTEGWINRYSEPFPGR
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                                                                                     YGKNSTLQQVKPVINATSRGLVEWSEPLSQCHLRNYWDPDIPFANS--YIRLVFELFVVI
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Pred. No. 1.2e-22;
9; Mismatches 231;
                                                                                                                     TPPYPYRTTVDYLRLAGE---VI 516
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R; Matthews, P.
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A;Cross-references: EMB
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A; Residues: 1-790 < WIL>
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Similarity 22.0%; Pred. No. 4.4e-14;
55; Conservative 94; Mismatches 209;
                                                                                                                                                         LAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLL
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                                                                                                                                                                                                           QFTSLLLRLGADLNQRCYGAFFCADDQKASRTDSLEHEFVELTKNTNYTGSMYFGEYPLS
                                                                                                   LKCARLFPDSNLEA-----VLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRK
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                             FKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRK 465
                                                                                                                                      FAICMGQHDLFRMLLA---KKANLSAQDTNGNTALH-LCVIHD-
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hypothetical protein T10B10.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24772
R;Sims, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-519 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, A;Reference number: Z19934
A;Accession: T24772
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                                                 GSLNPNSVIANVVYGDKVD--HLEFFDGLIEEVLESKWETFGKKQLFMSLAGYIYFLAVF
 YL 430
                            TL 487
                                                                                                                                    SPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEE- 430
                                                                                                                                                                                                                   VKQMTYRFPKIVNDIFLSEEYYASVGLSPLHQAIVNEDLEMVYFLCRKGADVHQRCYGSF
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                                                                                                          TPLALAARLAKKHIYDLILE---CDMDI--
                                                                                                                                                                 ADPNMPDTNGNTVLH--------LTVIHDLPEMFMLAVELGANLH-VRNNLKL
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                                                                              ----ASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIF 485
                                                                                                                                                                                         ADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGL
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                                                                                                                                                                                                                                                                                                                             7.2%; Score 278; DB 2; Length 519; 29.5%; Pred. No. 7.9e~12; tive 36; Mismatches 115; Indels
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                                                                                                            -SWRYGPVVCKAYPLNDVDTINESD
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    --QNRPEFSTIFMSPLKTTVMMIGEFEFTGIFHGDETTHAEKMFGPAHTAVACALFFFFC 1030
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosldues: 1-1188 <WIL>
A;Residues: 1-1188 <WIL-
A;Residues: 1-1188 <WIL
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A;Introns: 147/2; 473/3; 500/1; 529/1; 584/2; 688/2; 839/3; 975/3; 1132/3
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Local Similarity 20.3%; Pred. No. 4.1e-06;
hes 152; Conservative 98; Mismatches 250;
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SCRDSETFSTFLLDLFKLTIGM------
                                                                                                                 FGIFVVMFVDIV-KTFFRFFPVFVLFIIAFSSSFYVIL-
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     -GD----LEMLSSTKYPVVFIILLVTYI 703
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R;Preutz, K.D.; Noeller, J.K.; Krause, E.; Goebel, A.; Schulz, I. Biochem. Biophys. Res. Commun. 240, 167-172, 1997
A;Title: Expression and characterization of a trpl homolog from ra A;Reference number: JC5807; MUID:98042538; PMID:9367904
A;Accession: JC5807
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-828 -PRE>
A;Experimental source: brain
C;Comment: This protein participates in store-operated Ca2+ entry
C;Superfamily: TRPC3 protein
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C;Species: Rattus norvegicus (Norway
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Pred. No. 3.6e-05;
0; Mismatches 240;
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A;Title: Identification of a Drosophila gene encoding a
A:Poforence number: JH0588; MUID:92232293; PMID:1314616
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A;Cross-references: UNIPROT:P48994;
A;Experimental source: head
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C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Ju
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Neuron 8, 631-642, 1992
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                           -SNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 145.5; 1
Pred. No. 0.05
99; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - PLLLEEKKFLLAVERGDMPNVRRILQKALRHQHININC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:M88185;
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                                                                                                                                                                                                 ----MKFLIHASSYLFFLFILILVS-----
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                                                                                                                                                EVITLETGYLFFFTNIKDLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -PH--
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                                                  -AYLAVMVF
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194

309

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134

267 74

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436

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580 450

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A;Cross-references: EMBL:X89066; NID:g1019786; PID:g1019787
C;Superfamily: TRPC3 protein
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R;Wes, P.D.; Chevesich, J.; Jeromin, A.; Rosenberg, C.; Stetten, G.; Montell, Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995
A;Title: TRPC1, a human homolog of a Drosophila store-operated channel. A;Reference number: I38361; MUID:96003837; PMID:7568191
A;Accession: I38361
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-810 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 04-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRPC1 protein -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               581
                       444
                                                                                                                                                            279 ARQCKMFAKDLLAQAR--NSRELEVILNHTSSDEPLDKRGLLEERMNLSRLKLAIKYN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 PQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKK----RLTDEEFREP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71
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ENRHEMLAVEPINELLRDKWRKFGAV-----SFYINVVSYLCAMVIFTL-TAYYQPLEG 496
                                                                                                               GIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVYNSKI 443
                                                                                                                                                                                                                                                         YRCLASPALIMLTEEDP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----PGLPPSWAAMMAALYPSTDLSGASSSSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGPGDGRPNLRMKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSKESKHIWK 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSQSLFWASFGMVGLDDFELSGIKSYTRFWGLLMFGSYSVINVIVLLNLLIAMMSNSYAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT-----IGMGDLEMLSSTKYPVVF-IILLVTYIILTFVLLLNMLIALMGETVGQ 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFACGLNQLLWYFAAL----EKSKCYV--LPGGEADWGSHGDSCMKWRRFG----NLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYASALVSLLNPCANMKVCNEDQTNCTVPTYP-----SCRDSETFSTFLLDLFK 675
                                                                                                                                                                                                                                                                                                 AACTNOPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIAD------NTRENT 339
                                                                                                                                                                                                                                                                                                                                              ----APVILAAHRNNYEILTMLLKQDVSLPKPHAVGCECTLCSAKNKKDSLRHSRFRLDI 233
                                                                                                                                                                                                                                                                                                                                                                                       YRGQTALHIAIERRCKHYVELLVAQGADV---HA-QARGRFFQPKDEGGYFYFGELPLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STGK---TCLP-----KALLNLSNGRNDTIPVLLD-----IAERTGNMREFINSPFRDIY 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSSPSSSPNEVMALK------DVREVKEENTLNEKL-FLLACDKGDYYMVKKILEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDNKRWRKKIIEKQ 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PG----IPGPRAEAAVGTTHPFSSPGAWLGSGSGS----GPVGAPPPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDEHSDTEWK 684
                                                                                                                                                                                                         KFVTKMYDLLLLKCARLFPDSNLEAVLNND-
                                                                                                                                                                                                                                                                                                                                                                                                                                      SSGDLNINCVDVLGRNAVTITIENENLDILQLLLDYGCQKLMERIQNPE---YSTTMDV- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 126; Mismatches 315; Indels 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --ALVLGWMNALYFTRGLKLTGTYSI-----MIQKILFK---DLFRFLLVYLLFMI 626
                                                                  -QKEFVSQSN----CQQFLNTVW----FGQMSGYRRKPTCKKIMTVLTVGIF----
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18.1%; Pred. No. 0.11;
                                                                                                                                                                                                                                                         ----ILRAFELSADLKELSLVEVEFRNDYEEL
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                                                                                                                                                                                                              ---GLSPLMMAAKTGKI 383
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R;Shinn, P.; Buehler, B.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, eologis, A.; Ecker, J.R. submitted to the EMBL Data Library, January 1998
A;Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.
A;Reference number: Z14208
A;Accession: T00894
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F21B7.8 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear ceres) (;Species: Arabidopsis thaliana (mouse-ear ceres) (;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004 (;Date: 12-Feb-1999 #sequence_revision) (2-Feb-1999) #text_change 09-Jul-2004 (;Accession: T00894)
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A; Introns: 229/1; 411/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                            190
                                                                                                                                                                                                                                                                                                                                      130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 GSTADLDGLLPFLLTHKKRLTDEEFREPSTGKTCLPKA--LLNLSNGRNDTIPVLLDIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    704 ILTFVLLLNMLIALMGETVGQVSKESKHIWK 734
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    424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 RTGN------MREFINSPF----RDIYYRGQTALHIAIERRCKHYVELLV---
                                                                                                                                                                                                                                                                                                                                                                                                                               70 NQGNSILHIAAALGHVHIVEFIISTFPNLLQNVNLMGETTLHVAARAGSLNIVEILVRFI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-616 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSLSDPDQWTIF-----KDKDESEIMNPAI--LCAVRAGDKVSLLKRINDDVKVTQRLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQQSNDTFHSFIGTCFAL----FWYIFSLAHVAIFVTRFSYGEELQSFVGAVIVGTYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGPLQISMGQML-QDFGKFLGMFLLVLFSFTIGLTQLYDKGYTSK----EQKDC-VGIFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYP 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSIYLATFALKVVAHNKFHDFADRKDWDAFHPTLVAEGLFAFANVLSYLRLFFMYTTSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTMGPALERIDYL-----LILWIIGMI--WSDIKRLWYE---GLED-FLEESRNQLSFVM
                                                   HVRIIKEFLKHCPDSRELLNNQCQNIFHVAAIAGKSKVVKYLLKLDEGKRMMNEQDINGN
                                                                                                                                                                                                                                            AGYHELVLKMLESSSSPSILASMFSGKSVIHAAMKANRRDILGIVLRODPGLIELRNEEG
                                                                                                                                                                                                                                                                                        --FGELPLSLAACTNQPHIVNYLTE----NPHKKADMR-----RQD-----SRG
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                                                                                                                                              RTCLS--YGASMGCYEGIRYILAEFD----KAA-----SSLCYVADDDGFTPIHMAAKEG
                                                                                                                                                                                          NTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTG
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    ----LDTCGEEASVLEILVYNSKIENR---HEMLAVEPINELLRDKWRKFGAVSFYINVV 476
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                                                                                                  -REVIDEDIRH-----LSRKFKDWAY-----GPVYSSLYDLSS-
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Search	Дb	Q	ДЪ	γQ	DЬ	Ş	ф	Ş	σb
Search completed. December 3 2004 22.27.25	576 MILLIIPYA 583	622 LLEMIGYA 629	526 KAFRIALPLILTAVVSMMMASVAGLTLVVSDLPWLSHLVLAIDSAFLVFL 575	578 MVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFLLVY 621	469TLPGGYMSSAPHIGMAALVNKLNEKVFILLINNIAMCTSVVTVMALIMAQIGDALITK 525	525 FFTINIKOLFMKKCPGVNSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAV 577	411 KRLIWMALVSAGAPHGPNLIPLTVSQSSKQSPERYKDSVNTLMVTATLVATVTFAAGL 468	477 SYLCAMVIETLTAYYOPLEGTPPYPYRTTVDYLRLAGEVITLETGVLF 524	359 TPLHLATKHRYPIVNMLTWNDGINLRALNNEGFTALDIAETMKDNNAYV-LY 410

Search completed: December 2, 2004, 22:27:35 Job time : 49 secs

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Result
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Maximum Match 100%
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Maximum DB
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2: uniprot_trembl:*
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45	44	43	42	41	40	39	38	37	36	35	34	G.	32
1287	1298.5	1304.5	1304.5	1304.5	1304.5	1309	1309	1312	1316	1321	1322	1322	1324
33.4	33.7	33.8	33.8	33.8	33.8	33.9	33.9	34.0	34.1	34.2	34.3	34.3	34.3
764	764	756	756	756	756	791	765	790	790	791	762	761	761
N	N	N	N	N	N	N	N	N	N	N	N	N	N
Q9Y670	Q9Y5S1	AAS66752	Q99K71	Q9WTR1	Q6JGX2	Q8NET8	Q8NET9	QBNDW7	Q8NFH2	Q8K424	8 IML60	8HXÖ6Ö	Q9WUD2
Q9y670 homo sapien	Q9y5s1 homo sapien	Aas66752 f-11 rat/	Q99k71 mus musculu	09wtr1 mus musculu	Q6jgx2 f-11 rat/mo	Q8net8 homo sapien	Q8net9 homo sapien	Q8ndw7 homo sapien	Q8nfh2 homo sapien	Q8k424 mus musculu	Q9jmi8 rattus norv	Q9qyh8 rattus norv	Q9wud2 rattus norv

## ALIGNMENTS

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RESULT 1
QB6YZ6
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Best Local Similarity
Matches 736; Conser
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005261; F:cation channel activity; IEA.
GO; GO:000612; P:cation transport; IEA.
InterPro; IPR002110; ANK.
InterPro; IPR002111; Cat channel TrpL.
InterPro; IPR008996; Cytok IL1 like.
InterPro; IPR008996; Cytok IL1 like.
InterPro; IPR008979; TRPChannel.
InterPro; IPR008979; TRPChannel.
InterPro; IPR008979; TRPChannel.
InterPro; IPR008348; Vanil_receptor.
R InterPro; IPR008348; Vanil_receptor2.
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Pfam; PF00023; Ank; 3...

Pfam; PF000520; Ion trans; 1.

PRINTS; PR011615; ANKYRIN.

PRINTS; PR01769; VRLZRECEPTOR.

PRINTS; PR01769; VRLZRECEPTOR.

SMART; SM00248; ANK; 3.

TIGREAMS; TIGR00870; trp; 1.

PROSITE; PS50088; ANK REPEAT; 1.

PROSITE; PS50088; ANK REPEAT; 1.

PROSITE; PS50097; ANK REPEAT; 1.

PROSITE; PS50098; ANK REPEAT; 1.
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SUZUKI M.,
SUDMITTED (JAN-2003) to the EMBL/GenBank/DDBJ
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Mammalia; Eutheria; Primates;
NCBI TaxID=9806;
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01-JUN-2003 (TrEMBLrel. 24, L
01-MAR-2004 (TrEMBLrel. 26, L
Hypothetical protein TRPV-SV.
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                                                                                                       MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP
GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
                                                               MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP
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100.0%; Pred. No. 4e-233;
tive 0; Mismatches 0
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24, Last sequence update)
26, Last annotation update)
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                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Pr:
NCBI TaxID=9806;
[1]
                                                                                                                                                                                                                                                                                                                                                                            QBNDY7; PRELIMINARY; PRT; 871 AA.
QBNDY7; QBNDY7;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Vanilloid receptor-like channel 2.
Name=VRL2;
SEQUENCE FROM N.A.

MEDLINB=22107054; PubMed=12077606;

MEDLINB=22107054; PubMed=12077606;

Smith G.D., Gunthorpe M.J., Kelsell R.B., Hayes P.D., Reil Facer P., Wright J.E., Jerman J.C., Walhin J-P., Ooi L., E Charles K.J., Smart D., Randall A.D., Anand P., Davis J.B.

"TRPV3 is a temperature-sensitive vanilloid receptor-like Nature 418:186-190(2002).

BMBL, AJ296305; CAC82937.1; -.

Genew, HGNC:18083; TRPV4.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005261; F:cation channel activity; IEA.
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OR GO; GO:0004872; F:receptor activity; IEA.

R GO; GO:0006812; P:cation transport; IEA.

R InterPro; IPR002111; Cat channel TrpL.

R InterPro; IPR002111; Cat channel TrpL.

R InterPro; IPR002111; Cat channel TrpL.

R InterPro; IPR008996; Cytok_IL1_like.

R InterPro; IPR008996; Cytok_IL1_like.

R InterPro; IPR008347; Vanil_receptor.

R InterPro; IPR008347; Vanil_receptor.

R InterPro; IPR008348; Vanil_receptor2.

Pfam; PF00023; Ank; 3.

OR Pfam; PF00023; Ank; 3.

OR PfAm; PF00023; Ank; 3.

OR PRINTS; PR01469; VRL2RECEPTOR.

PRINTS; PR01769; VRL2RECEPTOR.

PRINTS; PR01769; VRL2RECEPTOR.

OR PRINTS; PR000408; ANK; 3.

R TIGRPAMS; TIGR00870; ttp; 1.

OR PROSITE; PS50088; ANK, REPEAR; 1.

OR PROSITE; PS50089; ANK_REP_REGION; 1.

ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;

RW Transmort.
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InterPro; IPR002111; Cat channel TrpL.
InterPro; IPR008996; Cytok II1 like.
InterPro; IPR008997; Ion trans.
InterPro; IPR004729; TRPChannel.
InterPro; IPR008347; Vanil receptor.
InterPro; IPR008348; Vanil receptor2.
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Nat. Cell Biol. 2:695-702(2000).
EMBL; AF258465; AAG16127.1;
GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0015281; F:nonselective cation channel
GO; GO:0006816; P:calcium ion transport; NAS.
ThterPro. TDBN0710. NAW
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MEDLINE=20482174; PubMed=11025659;
Strotmann R., Harteneck C., Nunnen
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Mammalia; Eutheria;
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01-DEC-2001 (TrEMBLrel. 19
01-DEC-2001 (TrEMBLrel. 20
01-MAR-2004 (TrEMBLrel. 20
Vanilloid receptor like c
          Pfam; PF00023; Ank; 3.

Pfam; PF000520; Ion trans; 1.

Pfam; PF01415; ANKYRIN.

PRINTS; PR01768; TRPVRECEPTOR.

PRINTS; PR01769; VRL2RECEPTOR.

PRINTS; SM0248; ANK; 3.

TIGRFAMS; TIGR00870; trp; 1.

PROSITE; PS50088; ANK REPEAT; 1.

PROSITE; PS50297; ANK REP REGION; 1.

ANK repeat; Ion transport; Ionic cha
                                                                                                                                                                                                                                                                                           SEQUENCE
[1]
                                                                                                                                                                            InterPro; IPR002111; ANK.
InterPro; IPR002111; Cat channel TrpL.
InterPro; IPR00896; Cytōk III like.
InterPro; IPR0089821; Ion trans.
InterPro; IPR004729; TRPChannel.
InterPro; IPR004347; Vanil receptor.
InterPro; IPR008348; Vanil_receptor2.
                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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Primates;
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19, Last s
26, Last a
channel-2.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
               channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    871
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             Receptor;
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Best Local S
Matches 736
Name=VROAC;
Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
NCBI_TaxID=9606;
[1]
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                                                                                                                        Q9HBA0 PRELIMINARY; PRT; 871 AA.
Q9HBA0;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Vanilloid receptor-related osmotically activated ch
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                                               Primates;
                                                                  Chordata;
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Pred. No. 4.1e-233;
                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005261; F:cation channel activity; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0006812; P:cation transport; IEA.

DR InterPro; IPR002111; Cat channel TrpL.

DR InterPro; IPR002111; Cat channel TrpL.

DR InterPro; IPR00896; Cytōk IL1_lTke.

DR InterPro; IPR008341; Ion trans.

DR InterPro; IPR008348; Vanil receptor.

DR InterPro; IPR008348; Vanil receptor2.

DR InterPro; IPR008348; Vanil receptor2.

DR Pfam; PF00520; Ion trans; 1.

DR Pfam; PF00520; Ion trans; 1.

DR Pfam; PF00520; Ion trans; DR Pfam; PF00520; Ion trans.

DR Pfam; PF00520; Ion trans; DR Pfam; PF00520; Ion trans.

DR Pfam; PF00520; Ion trans; DR Pfam; PF00520; Ion trans.

DR Pfam; PF00520; Ion trans.

DR PFAMTS; PR01769; VRLARECEPTOR.

DR PRINTS; PR01769; VRLARECEPTOR.

DR PRINTS; PR01769; VRLARECEPTOR.

DR PRINTS; PR01769; VRLARECEPTOR.

DR PRINTS; PR01769; VRLARECEPTOR.

DR PROSITE; PS00248; ANK; 3.

DR PROSITE; PS00284; ANK; REPEAT; 1.

DR PROSITE; PS00287; ANK_REPEAT; 1.

DR PROSITE; PS0028; ANK_REPEAT; 1.

DR PROSITE; PS0028; Ion transport; Ionic channel; Receptor; Transmembrane; KW Mrsnerort
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MEDLINE=20531888; PubMed=11081638;

Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M.,

Sali A., Hudspeth A.J., Friedman J.M., Heller S.;

"Vanilloid receptor-related osmotically activated che candidate vertebrate osmoreceptor.";
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   NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG
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Pred. No. 4.7e-233;
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RMED; MGI:1926345; Trpv4.

RGO; GO:00050262; F:calcium channel activity; IDA, GO:0005034; F:camous activity; IDA, GO; GO:0005034; F:camous activity; IDA, GO; GO:0007231; P:osmosensory signaling path GO; GO:0007231; P:osmosensory signaling path GO; GO:0007231; P:osmosensory signaling path GO; GO:00070103; P:vasopressin secretion; IME GO; GO:0030103; P:vasopressin secretion; IME GO; GO:0030103; P:vasopressin secretion; IME GO; GO:0030103; P:vasopressin secretion; IME InterPro; IPR002111; Cat channel TrpL.

R InterPro; IPR008311; Cat channel TrpL.

R InterPro; IPR008321; Ion trans.

R InterPro; IPR008321; Ion trans.

R InterPro; IPR008346; Vanil receptor.

R Pfam; PP00502; Jon trans; 1.

PFAm; PP00502; Jon trans; 1.

PRINTS; PR01768; TRPVRECEPTOR.

PRINTS; PR01768; TRPVRECEPTOR.

PRINTS; PR01768; TRPVRECEPTOR.

PROSITE; PS50088; ANK REPERSION; 1.

PROSITE; PS50088; ANK REPERSION; 1.

PROSITE; PS50297; ANK_REPERSION; 1.
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01-MAR-2001 (TrEMBLrel. 16, Cre
01-MAR-2001 (TrEMBLrel. 16, Las
01-MAR-2004 (TREMBLrel. 26, Las
Transient receptor potential p
Name=Trpv4; Synonyms=Trp12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wissenbach U., Boedding M., Freichel "Trp12, a novel Trp related protein FEBS Lett. 485:127-134(2000).
EMBL; AJ296078; CAC20703.1; -.
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Mammalia; Eutheria; Rodentia;
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                                                                  MADPGDGPRAAPGEVAEPPGDESGTSGGEAFPLSSLANLFEGEEGSSSLSPVDASRPAGP
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ilarity 95.7%;
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1 protein 12.
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Pred. No. 1.2e
l6; Mismatches
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10116;
iiedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Sali A., Hudspeth A.J., Friedman J.M., Heller S.;
"Vanilloid receptor-related osmotically activated ch candidate vertebrate osmoreceptor.";
Cell 103:525-535(2000).
EMBL; AF263521; AAC38027.1; -.
GO; GO:001621; C:integral to membrane; IEA.
GO; GO:0005261; F:cation channel activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
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                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Kidney;
MEDLINE-20531888; PubMed-11081638;
                                                                                                                                                                                                                                                                                                                                            Name=Vroac;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVGQVSKBSKHIWKLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSLFVDGSFQLLYFIYSVLVVVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALHIAIERRCKHYVELLVAQGADVHAQARGREFQPKDEGGYFYEGELPLSLAACTNQPHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Rodentia;
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Sciurognathi; Muridae;
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Pfam; PF00520; Ion_trans; 1.

PRINTS; PR01769; TRPVRECEPTOR.

PRINTS; PR01769; VRL2RECEPTOR.

PRNART; SM00248; ANK; 3.

TIGRPAMs; TIGRO0870; trp; 1.

PR0SITE; PS50088; ANK REPERAT; 1.

PR0SITE; PS50088; ANK REP_REGION; 1.

PROSITE; PS50297; ANK_REP_REGION; 1.
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InterPro; IPR004729; TRPChannel.
InterPro; IPR00847; Vanil_receptor.
InterPro; IPR008348; Vanil_receptor2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0006812; P:cation transport; InterPro; IPR002110; ANK. channel Trp InterPro; IPR008996; Cytok_Itl_like.
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                                                                   TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQINCTVPTYPSC
                                                                                                                 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
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TVGQVSKESKHIWKLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.7%; Score 3693; I
95.5%; Pred. No. 1.66
tive 17; Mismatches
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R GO; GO:0005262; F:calcium channel activity; IDA.

R GO; GO:0005262; F:calcium channel activity; IDA.

R GO; GO:0005034; P:osmosensor activity; IDA.

R GO; GO:0007231; P:osmosensory signaling pathway; IDA.

R GO; GO:0007231; P:osmosensory signaling pathway; IDA.

R GO; GO:0047484; P:regulation of response to osmotic stress; IMP

R GO; GO:0030103; P:vasopressin secretion; IMP.

R InterPro; IPR002110; ANK.

R InterPro; IPR002111; Cat channel TrpL.

R InterPro; IPR003996; Cytok II1 like.

InterPro; IPR005821; Ion trans.

R InterPro; IPR005821; Ion trans.

R InterPro; IPR005841; Vanil receptor.

InterPro; IPR008347; Vanil receptor.
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Best Local Similarity
Matches 703; Conserv
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Pfam; PF000520; Ion trans; 1.

Pfam; PF000520; Ion trans; 1.

PRINTS; PR01768; TRPVRECEPTOR.

PRINTS; PR01769; VELZRECEPTOR.

SMART; SM00248; ANK; 3.

TIGRFAMS; TIGR00870; trp; 1.

PROSITE; PS50088; ANK_REPEAT; 1.

PROSITE; PS50297; ANK_REPEAT; 1.

PROSITE; PS50297; ANK_REP REGION; 1.

ANK repeat; Ion transport; Ionic channel; Transmembrane; ANK repeat; 10n transport; 28228D554083F00A CRC64;
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EMBL; AF208026; AAG17543.1; -.
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STRAIN=129/SVEV;
MEDLINE=20482114; PubMed=11025659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTRPC4 cation channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN
                                                 GDGRPNLRMKFQGAFRKGVPNPIDLLESTRYESSVVPGPKKAPMDSLFDYGTYRHHPSDN
                                                                                                                                                                                                                                               <u>WADPGDGPRAAPGEVAEPPGDESGTSGGEAFPLSSLANLFEGEEGSSSLSPVDASRPAGP</u>
ALHIAIBERCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
                                                                                                                KRWRRKVVEKOPOSPKAPAPOPPPILKVFNRPILFDIVSRGSTADLDGLLSPLLTHKKRL
                                                                                                                                  KRWRKKIIEKQPQSPKAPAPQPPPILKVENRPILFDIVSRGSTADLDGLLPFLLTHKKRL
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                                                                                                                                                                                                                                                                                                              95.6%; Score 3689; DB 2; 95.5%; Pred. No. 2.8e-224; ive 16; Mismatches 17;
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A Suzuki M., Mizuno A., Kodaira K., Imai M.;

"Impaired pressure sensation in mice lacking TRPV4.";

J. Biol. Chem. 278:22664-22668 (2003).

R EMBL; AB021875; BAA83731.2;

R MGD; MGI:1926945; Trpv4.

R GO; GO:0005034; F:csmosensor activity; IDA.

R GO; GO:0005034; F:csmosensor activity; IDA.

R GO; GO:0005034; F:csmosensor activity; IDA.

R GO; GO:0005034; F:csmosensor sclinity response; IMP.

R GO; GO:0007031; P:hyperosmotic salinity response; IMP.

R GO; GO:0007231; P:osmosensory signaling pathway; IDA.

R GO; GO:0007231; Cat channel TrpL.

R InterPro; IPR002111; Cat channel TrpL.

R InterPro; IPR008996; Cytok_II1_like.

R InterPro; IPR008996; Cytok_II1_like.

R InterPro; IPR008996; Cytok_II1_like.

R InterPro; IPR008347; Vanil_receptor.

R InterPro; IPR008347; Vanil_receptor2.

R Ffam; pF00023; Ank; 3.

R Pfam; pF00023; Ank; 3.

R Pfam; PF00023; Ank; 3.

R PRINTS; PR01768; TRPVRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Kidney;
MEDLINE=22692536; F
Suzuki M., Mizuno F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; H
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9EQZ4;
Q9EQZ4;
01-MAR-2001
01-MAR-2001
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ion channel
Name=Trpv4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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1 (TrEMBLrel.
4 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=12692122;
A., Kodaira K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
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Last sequence
Last annotation
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; Murinae; Mus
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RESULT
Q9ERZ7
ID Q9
AC Q9
DT 01
DT 01
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DT 01
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DT Va

PRELIMINARY;

873 AA

10

Q9ERZ7; Q9ERZ7; 01-MAR-2001 01-MAR-2001 01-MAR-2004 Vanilloid re

)1 (TrEMBLrel. 16, Created)
)1 (TrEMBLrel. 16, Last sequence update)
)4 (TrEMBLrel. 26, Last annotation update)
receptor-related osmotically activated ch

channel.

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Best Local Sim:
Matches 701;
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SMART; SM0248; ANK, 3.
TIGREAMS; TIGR00870; trp; 1.
PROSITE; PS50088; ANK REPEAT; 1.
PROSITE; PS50299; ANK REP REGION; 1.
ANK repeat; Ion transport; Ionic channel; Transmembrane;
BAUK repeat; Ion transport; Jonic channel; Transmembrane;
SEQUENCE 871 AA; 98060 MW; 3285AE576D32DD95 CRC64;
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                               RDSETESTFLLDLEKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE
TVGQVSKESKHIWKLQ
          TVGQVSKESKHIWKLQ
                                                               TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC
                                                                                                NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVEALVLGMMNALYFTRGLKLTG
                                                                                                                                LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC
                                                                                                                                                                                                NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD
                                                                                                                                                                                                                                                                 LSSLDTCGEEVSVLEILVYNSKI
                                                                                                                                                                                                                                           VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLLKCARLFPDS
                                                                                                                                                                                                                                                                                                 TDEEFRBSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT
                                                                                                                                                                                                                                                                                                                                MADPGDGPRAAPGEVAEPPGDESGTSGGEAFPLSSLANLFEGEEGSSSLSPVDASRPAGP
                                                                                                                                                                                                                                                                                                                                                                                                          MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP
                                                                                                                                                                                                                                  VNYLTENPHKKADMRRQDSRGNTVLHALVALADNTRENTKFVTKMYDLLLLKCSRLFPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           95.4%;
95.2%;
                  736
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 3681; D
Pred. No. 9e-2
17; Mismatches
                                                                                                                                                                 ENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC
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Best Local Similarity
Matches 697; Conserv
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InterPro; IPR002111; Cat channel TrpL.
InterPro; IPR008996; Cycok II1 like.
InterPro; IPR008996; Cycok II1 like.
InterPro; IPR008921; Ion trans.
InterPro; IPR004729; TRPChannel.
InterPro; IPR008347; Vanil receptor.
InterPro; IPR008348; Vanil receptor2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00023; Ank; 3.

Pfam; PF00520; Ion trans; 1.

PRINTS; PR01415; ANKYRIN.

PRINTS; PR01768; TRPVEECEPTOR.

PRINTS; PR01769; VRL2RECEPTOR.

SMART; SM00248; ANK; 3.

TIGRE00870; trp; 1.

PR0SITE; PS50088; ANK REPEAN; 1.

PROSITE; PS50297; ANK_REP_REGION; 1.

PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP33523 ARG28028.1; -.

EMBL; AP33522 ARG28028.1; -.

MGD; MGI:1926945; Trpv4.

GO; GO:0005262; F:calcium channel activity; IDA.

GO; GO:0005334; F:cosmosensor activity; IDA.

GO; GO:0042538; P:hypercosmotic salinity response; IMP.

GO; GO:0007231; P:cosmosensory signaling pathway; IDA.

GO; GO:0047494; P:regulation of response to osmotic stress;

GO; GO:0030103; P:vasopressin secretion; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE=20531888; PubMed=11081638;
Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
Sali A., Hudspeth A.J., Friedman J.M., Heller S.;
"Vanilloid receptor-related osmotically activated channel (VR-OAC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            candidate vertebrate osmoreceptor."; Cell 103:525-535(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Trpv4; Synonyms=Vroac;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transport.
SEQUENCE
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361
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                                                                                                                                         PGDGRPNLRMKFGRSAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHPS
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                                                                                                                                                                                                                                                                                                                                                                     WADPGDGPRAAPGEVAEPPGDESGTSGGEAFPLSSLANLFEGEESSYFSYPRWTASRPAG
                DSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSL
                                                            HIVNYLTENPHKKADMRRODSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCSRLFP
                                                                                                                      QTSLHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQP
                                                                                                                                                                                     RLTDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRG
DSNIETVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             873 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98596 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                             94.2%; Score 3636; DB 2;
94.4%; Pred. No. 6.3e-221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5DD87C92712B24EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
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Q96RS ID Q96RS AC Q96RS DT 01-DE DT 01-ME DE Vanil GN Name-e OS Homo OC Mamma OX NCB1 RA Derss EMBL, DR GO; OR EMBL, DR Intender GO; OR GRINN DR FRINN DR FROS KW Trann SQ SEQUI
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Best Local
                               Matches
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Q96RS7;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-MAR-2004 (TrEMBLrel. 2
                                                                                                                                                                                 Pfam; PF00023; Ank; 3.
Pfam; PF00520; Ion trans; 1.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR01768; TRPVESCEPTOR.
PRINTS; PR01769; VRLZRECEPTOR.
SMART; SM00248; ANK; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Derst C., Schafer M.K.;
Submitted (JUN-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TYENHITE). 19, Created)
01-DEC-2001 (TYENHITE). 19, Last sequence update)
01-DEC-4004 (TYENHITE). 26, Last annotation update)
Vanilloid receptor-like protein 2.
                                                                                                                    TIGREAMS; TIGRO0870; trp; 1.
PROSITE; PS50088; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION;
ANK_repeat; Ion transport; Ionic
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                               ; 899
                                               Similarity
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MKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDNKRWRKKII
                                                                                              803
                                 Conservative
                                                                                              A
A
                                                                                            91635 MW; AB329C595B325784 CRC64;
                                              100.0%;
                                                              90.0%;
                                 0;
                                                 Score 3472; DB 2; 1
Pred. No. 1.3e-210;
                                   Mismatches
                                                                                                                            channel; Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  803
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                                                              Length 803;
                                    Indels
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RESULT 12
Q8NG64
ID Q8NG66
AC Q8NG6
AC Q8NG6
DT 01-O(
DT 01-W)
DB OTRP
OS Homo
OC Euka
OC Mamm
OX NCB1
RN (CB1)
RP SEQ1
RN SUB
RY SEQ1
RD SEQ1
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SEQUENCE FROM N.A.

TISSUE-Abortic endothelium;

Xu F., Satch E., Iijima T.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ day

R EMBL; AB073669; BAC06573.1; -.

GO; GO:0016011; C:integral to membrane; IEA.

R GO; GO:0001521; F:cation channel activity; IEA.

R GO; GO:0005261; F:cation transport; IEA.

R GO; GO:0006812; P:cation transport; IEA.

R GO; GO:0006812; P:cation transport; IEA.

R GO; GO:0006812; Cation transport; IEA.

R InterPro; IPR002111; Cat channel TrpL.

R InterPro; IPR008996; Cytok III Ike.

R InterPro; IPR008996; Cytok III Ike.
                                                                                                                                                                                                                                                     Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                      Q8NG64;

Q1-QCT-2002 (TrEMBLrel. 22,

Q1-QCT-2002 (TrEMBLrel. 22,

Q1-MAR-2004 (TrEMBLrel. 26,

QTRPC4Deta cation channel.
                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                   Chordata; (; Primates; (
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Last seq
Last ann
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                                                                                                                                                                                                                                                                                                                       sequence update)
annotation update)
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; Homo.
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   RESULT 13
Q91XR5
ID Q91XR5
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SOWDRADAR
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Best Local Similarity
Matches 674; Conserv
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Pfam; PF00520; Ion trans; 1.

PRINTS; PR01761; TRPVPECEPTOR.

PRINTS; PR01769; VRLLRECEPTOR.

PRINTS; PR01769; VRLLRECEPTOR.

SMART; SM00248; ANK; 3.

PROSITE; PS50289; ANK REPEAT; 1.

PROSITE; PS50297; ANK REP REGION; 1.

ANK repeat; Ion transport; Ionic channel; Transmembrane;

ANK repeat; Ion transport; 10nic channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR008347; Vanil_receptor.
InterPro; IPR008348; Vanil_receptor2
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                                          RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE
                                                                                                                                 TVGQVSKESKHIWKLQ
                                                                                     AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV
                                                                                                                                                                                                                                                                      NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAXGPVYSSLYD
                                                                                                                                                                                                                                                                                                                  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS
                                                                                                                                                                                                                                                                                                                                                              ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSDADASRPAGP
                                                                                                                                                                                                                                       LSSLDTCGEEASVLEILVYNSKIENRHEMLAVBPINELLRDKWRKFGAVSFYINVVSYLC
                                                                                                                                                                                                                                                                                                                                                                                                                         TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREPINSPFRDIYYRGQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRWRKKIIEKOPOSEKAPAPOPPPILKVENRPILEDIVSRGSTADLDGLLPELLTHKKRL
 TVGQVSKESKHIWKLQ
                                                                                                                                                                                AMVIFTLTAYYOPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV
                                                                                                                                                                                                                                                                                                                                                                                                            TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRWRKKIIEKOPOSPKAPAPOPPPILKVFNRPILFDIVSRGSTÄDLDGLLPFLLTHKKRL
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91.6%;
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676
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Pred. No. 3.1e-210;
0; Mismatches 2;
                                                                                                                                                                                                                          NRHEMLAAEPINELLRDKWRKFGAVSFYINVVSYLC
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PRELIMINARY;

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R GO; GO:0005262; F:calcium channel activity; IDA.

R GO; GO:0005034; F:csmcsensor activity; IDA.

R GO; GO:0005034; F:csmcsensor activity; IDA.

R GO; GO:0004738; P:hyperosmctic salinity response; IMP.

R GO; GO:004728; P:csmcsensory signaling pathway; IDA.

R GO; GO:0030103; P:vasopressin secretion; IMP.

R InterPro; IPR002110; ANK.

R InterPro; IPR002111; Cat channel TrpL.

R InterPro; IPR008296; Cytok_ILl_like.

R InterPro; IPR008296; Cytok_ILl_like.

R InterPro; IPR004729; TRPChannel.

R InterPro; IPR004347; Vanil_receptor.

R InterPro; IPR008347; Vanil_receptor2.

R Pfam; PF00023; Ank; 3.

R Pfam; PF00023; Ank; 3.

R Pfam; PF000520; ION trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
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01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-MAR-2004 (TrEMBLrel. 26, Last annotation
Vanilloid receptor-like protein 2.
Name=Trpv4; Synonyms=Vrl2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO1415; ANKYRIN.

PRINTS; PRO1768; TRPVRECEPTOR.

PRINTS; PRO1769; VYLIZECEPTOR.

SMART; SM00248; ANK; 3.

SMART; SM00248; ANK; 1.

PROSITE; PS50088; ANK REPEAT; 1.

PROSITE; PS50088; ANK REPEAT; 1.

PROSITE; PS50088; ANK REPEAT; 1.

PROSITE; PS50297; ANK REPEAT; 1.

PROSITE; PS50297; ANK REPEAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Derst C., Schafer M.K.;
Submitted (JUN-2000) to the
EMBL; AF279672; AAK69486.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Kidney;
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645; Conserv
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                                                                                                                                                                                RCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHIVNYLTENP
                                                                                                                                                                                                                                                                                                                   RCKHYVELLVAQGADVHAQARGREFQPKDEGGYFYFGELFLSLAACTNQPHIVNYLTENP
                                                                                                                                                                                                                                                                                                                                                                                        STGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNWREFINSPFRDIYYRGQTSLHIAIER
                                                                                                                                                                                                                                                                                                                                                                                                                   STGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNWREFINSPFRDIYYRGQTALHIAIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEEFREP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKFQGAFRKGVPNPIDLLESTRYESSVVPGPKKAPMDSLFDYGTYRHHPSDNKRWRRKVV
BEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLT
                                                                                DGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGFVYSSLYDLSSLDTCG
                                                                                                             DGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCG
                                                                                                                                                                                                             HKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKOPOSPKAPAPOPPPILKVFNRPILFDIVSRGSTADLDGLLSFLLTHKKRLTDEEFREP
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nilarity 96.6%;
Conservative 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 3389; DB 2;
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Sciurognathi; Muridae;
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; Murinae; Mus
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              Pfam; PF00023; Ank; 3.

Pfam; PF00023; Ank; 3.

PRINTS; PR01415; ANKTRIN.

PRINTS; PR01468; TREVERCEPTOR.

PRINTS; PR01769; VRL2RECEPTOR.

PRINTS; PR01769; VRL2RECEPTOR.

SMART; SM00248; ANK; 3.

"TICRPAMS; TIGRO870; trp; 1.

PROSITE; PS50088; ANK REPEAT; 1.

PROSITE; PS50297; ANK REPEAT; 1.

PROSITE; PS50297; ANK REPEAT; 1.

PROSITE; PS00962; RIBOSOMAL S2 1; UNKNOWN 1.

PROSITE; PS00962; RIBOSOMAL S2 1; UNKNOWN 1.

ANK repeat; Ion transport; Tonic channel; Receptor; Transport; T
                                                                                                                                                                                                                                                                                                                           InterPro; IPR002110; ANK.
InterPro; IPR002111; Cat channel TrpL.
InterPro; IPR008996; Cytok III_like.
InterPro; IPR005821; Ion_trans.
InterPro; IPR002016; Peroxidase.
InterPro; IPR002016; Peroxidase.
InterPro; IPR004729; Richannel.
InterPro; IPR004729; Vanil receptor.
InterPro; IPR008347; Vanil receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9DFS3 PRELIMINARY; PKT; 852 Am.
Q9DFS3 101-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Vanilloid receptor-related osmotically activated ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=VR-OAC;
Name=VR-OAC;
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordatae; Galliformes; Phasianidae; Phasianin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF261883; AAG28026.1; -. GO:0016021; C:integral to membrane; IGO; GO:0005261; F:cation channel activity; IEA. GO; GO:0004872; F:receptor activity; IEA. GO; GO:0006812; P:cation transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            candidate vertebrate osmoreceptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liedtke W., Choe Y., Marti-Renom M.A., Bell A.M., Hudspeth A.J., Friedman J.M., Heller S.; "Vanilloid receptor-related osmotically activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20531888; Put
Liedtke W., Choe Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Cochlea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                             Vanil_receptor2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity;
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                                  Transmembrane;
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Matches 624
          Q8QFN9 PRELIMINARY; PRT; 843 AA.
Q8QFN9;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Vanilloid receptor-like protein.
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
UCBI TaxID=9031;
[1]
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TISSUE-Dorsal root ganglia;
TISSUE-Bate 200; PubMed=11853675;
MEDLINE=21842900; PubMed=11853675;
Jordt S.E., Julius D.;
"Molecular basis for species-specific
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Local 9
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SAALYLAGIEAYLAVMVEALVLGWMNALYETRGLKLTGTYSIMIQKILFKDLFRFLLVYL
                                                            HTLVEIADNTKDNTKFVTKMYNNILILGAKINPILKLEELTNKKGLTPLTLAAKTGKIGI
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nilarity 47.5%;
Conservative 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            %; Score 1604.5; DB 2; Length
%; Pred. No. 1.2e-92;
128; Mismatches 184; Indels
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Search Job ti	Дb	γQ	DЬ	γQ	뫄	γQ	ఠ
Search completed: December 2, 2004, 22:26:45 Job time : 206 secs	706 LQ 707	735 LQ 736	646 KFTIGMGDLEFTENYRFKSVFVILLVLXVILTYILLINMLIALMGETVSKIAQESKSIWK 705	675 KLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGETVGQVSKESKHIWK 734	594 VELLGESTAVVTLIEDDNEGODTNSSEYARCSHTKRGRTSYNSLYYTCLELF 645	623 LFMIGYASALVSLINPCANMKVCNEDQ-TNCTVPTYPSCRDSETFSTFLIDLF 674	534 SVVLYFCGQELYVASMVFSLALGWANMLYYTRGFQQMGIYSVMIAKMILRDLCRFMFVYL 593

GenCore version 5.1.6

## ALIGNMENTS

닭 capsaicin receptor - rat
N;Alternate names: vanilloid receptor subtype 1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004
C;Accession: T09054
R;Caterina, M.J.; Schumacher, M.A.; Tominaga, M.; Rosen, T.A.; Levine, J.D.; Julius, D. Nature 389, 816-824, 1997
A;Title: The capsaicin receptor: A heat-activated ion channel in the pain pathway.
A;Reference number: Z16539; MUID:98007969; PMID:9349813 Ś A;Cross-references: UNIPROT:035433; EMBL:AF029310; NID:g2570932; PIDN:AAC53398.1; PID:eA;Experimental source: dorsal root ganglion C;Keywords: ion channel; receptor A;Molecule type: mRNA A;Residues: 1-838 <CAT> A; Status: preliminary; translated from GB/EMBL/DDBJ Query Match 2.2%; Score 16; Best Local Similarity 100.0%; Pred. No. Matches 16; Conservative 0; Mismatci Mismatches 1.1e-07; hes 0; DB 2; Length 838 Indels ç, Gaps 0

Capsaicin receptor, VR1 - human
(c;Species: Homo sapiens (man)
(c;Decies: Homo sapiens (man)
(c;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004
(c;Accession: JC7621
R;Cortright, D.N.; Crandall, M.; Sanchez, J.F.; Zou, T.; Krause, J.E.; White, (Biochem. Biophys. Res. Commun. 281, 1183-1189, 2001
A;Title: The tissue distribution and functional characterization of human VR1.
A;Reference number: JC7621; MUID:21139751; PMID:11243859
A;Contents: Dorsal root ganglia

G

A;Map position: 17p13
C;Keywords: transmembrane protein
F;201-233/Domain: ankyrin #status
F;248-280/Domain: ankyrin #status
F;333-365/Domain: ankyrin #status A;Molecule type: mRNA A;Residues: 1-839 <COR> A;Cross-references: UNIPROT:Q9H304; GB:AF196175 C;Comment: This receptor, a transmembrane protein with many phosphorylation sites, its integrative activation by several noxious stimuli, and plays an important role A; Gene: vrl

in

predicted <ANK1>
predicted <ANK2>
predicted <ANK3>

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F;433-455/Domain: t
F;477-495/Domain: t
F;508-531/Domain: t
F;543-569/Domain: t
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Nucleic Acids Res. 26, 5190-5198, 1998
A;Title: Structure and organization of the mitochondrial genome
A;Reference number: A58930; MUID:99030526; PMID:9801318
A;Accession: H58933
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F;624-644/Region:
F;656-684/Domain:
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C;Genetics:
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A; Residues: 1-79 < ARN>
                                                                                                                                                                                                                                                         A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: F95116
                                                                                                                                                                                                                                                                                                                                                        R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; on, J.D.; Umayam, L.A.; White, O.; Salzberg, nson, T.; Hickey, E.K.; Holt, I.E.
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                                                                                                                                                        A; Experimental source:
                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-143 < KUR>
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Best Local
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Experimental source: strain TIGR4
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                                                      Score 8; DB 2; Pred. No. 5.9;
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S.L.; Lewis,
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Radune, D.; Holtzapple,
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                                                                                  R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes: Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten:
                                          A;Reference number: AD3252; PMID:11756688
A;Accession: AC3408
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A;Status: preliminary

C; Accession: AC3408

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J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae St
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: D97986
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C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: D97986
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                                                                                                                                                                                                           Ride Wergiiosse, P.; Lintermans, P.; Limet, J.N.; Cloeckaert, J. Bacteriol. 177, 1911-1914, 1995
A;Title: Cloning and nucleotide sequence of the gene coding for A;Reference number: A56152; MUID:95204367; PMID:7896724
A;Accession: A56152
A;Status: preliminary
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A; Residues: 1-143 < KUR>
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A; Residues: 1-213 < DEA>
A; Cross-references: UNI
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C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change
C;Accession: A56152
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7 LVIVSAAL 14
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Pred. No. 8.2;
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: C64538
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C;Accession: H69002
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T., Çiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
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A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytochrome-c oxidase (EC 1.9.3.1) chain fixP - Helicobacter pylori (strain 26695) C;Species: Helicobacter pylori (C;Species: Helicobacter pylori (C;Datce: 109-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
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C; Superfamily:
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;Cross-references: UNIPROT:Q45321;
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8; Conserv
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%; Pred. No. 8.2
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Watthey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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glycogen b C;Species:

biosynthesis proteins: Streptococcus pneum

pneumoniae

GlgD

[imported] -

Streptococcus

pneumoniae

(strain

TIGR4)

143

A95130 RESULT 12

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DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic
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                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein alr5117 [imported] - Nostoc sp. (strain PCC C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: press.
A;Molecule type: DNA
A;Residues: 1-334 <KUR>
A;Residues: 1-334 <KUR>
A;Cross-references: UNIPROT:Q8YTF7; GB:BA000019;
A;Cross-references: UNIPROT:Q8YTF7; GB:BA000019;
                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8YM24; GB:BA000019; PIDN:BAB76816.1; PID:g17134255; GSPDB A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-341 < KUR>
                                                                                                                                                                                                                                                                    A; Reference number: AB1807; A; Accession: AE2445
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              serine/threonine kinase [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 C;Accession: AI2150
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Matches 8; Conserv
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 136
                               286
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                                                                 Similarity
8; Conserv
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8; Conserv
 ELPLSLAA
                               ELPLSLAA 293
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                                                                                                                            alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
                                                                 Conservative 0;
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                                                                                                                                                                                                                                                                                                                                   S.; Sugimoto,
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                                                                                                                                                                                                                                                                                  Sequence of the Filamentous Nitrogen-fixing Cyanobacterium 7; MUID:21595285; PMID:11759840
                                                                               1.1%; Score 8;
100.0%; Pred. No
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                                                                               No.
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12;
                                                                                               DB 2;
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                                                               0;
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                                                                 Indels
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, M.; Yasuda,
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09-Jul-2004
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A;Status: preliminary

A; Molecule type: DNA

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required for glycogen biosynthesis [imported] - Streptococcus pneumoniae (strain R6) C;Species: Streptococcus pneumoniae (c;Species: Streptococcus pneumoniae) (c;Species: Streptococcus pneumoniae) (c;Species: Streptococcus pneumoniae) (c;Species: Streptococcus pneumoniae) (c;Species: Strain R6. A;Reference number: A97872; MUID:21429245; PMID:11544234 A;Accession: G98000
                                                                                               R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Restaues: 1-379 <KUR>
A;Cross-references: UNIPROT:Q8DPS4; GB:AE007317; PIDN:AAK99835.1; PID:g15458649; GSPDB:G
C;Genetics:
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                                                                                                                                                                                                      probable antigen, p83/100 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: F71317
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                                                         A; Reference number: A71250; A; Accession: F71317
                                                                                                                                                                                                                                                                                                                   RESULT 14
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             Molecule type: DNA
                                   Status: preliminary; nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                           31 FPLSSLAN 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8;
1-484 <COL>
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8; Conser
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larity 100.0%;
Conservative 0;
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                                                                                  sequence of Treponema pallidum, the
so; MUID:98332770; PMID:9665876
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; Pred. No. 13
0; Mismatches
                                        sequence not shown;
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360 GSTADLDG 161 GSTADLDG 168

367

Search completed: December Job time : 45 secs

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x;rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heicon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: A95130
A;Status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:083499; GB:AE001225; GB:AE000520; NID:g3322775; PIDN:AAC6547
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0486
                                                                         A;Map position: megaplasmid pHV3
A;Genome: plasmid
A;Note: expressed during exponential g
C;Superfamily: NAD-dependent aldehyde
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004 C;Accession: T44987
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                                                                                                                                                                                  A;Residues: 1-496 <FAR>
A;Cross-references: UNIPROT:034184; EMBL:U95374; PIDN:AAB71806.1
A;Experimental source: strain DS2
C;Genetics:
                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                            A; Reference number: Z22886
A; Accession: T44987
                                                                                                                                                                                                                                                                                                                                                   R;Farahani, R.; Imbeault, J.C.; St Jean, A.; Chan, C.C.Y.; Allard, submitted to the EMBL Data Library, March 1997
A;Description: Hereditary instability of the megaplasmid pHV3, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                         aldehyde dehydrogenase (BC 1.2.1.-) [imported] - Haloferax volcanii megaplasmid C;Species: Haloferax volcanii
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     GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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## ALIGNMENTS

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61 GDGRENLRMKFQGAFRKGVÞNPIDLLESTLYESSVVÞGÞKKAÞMDSLFDYGTYRHHSSDN 12	1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60 	Query Match 99.2%; Score 736; DB 2; Length 853; Best Local Similarity 100.0%; Pred. No. 0; Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps	Ol-JUN-2003 (TrEMBLrel. 24, Created) Ol-JUN-2003 (TrEMBLrel. 26, Last sequence update) Ol-JUN-2003 (TrEMBLrel. 26, Last sequence update) Ol-MAR-2004 (TrEMBLrel. 26, Last annotation update) Name=TRPV-SV; Homo sapiens (Human). Exkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; Il SEQUENCE FROM N.A. Suzuki S.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases. I2] SEQUENCE FROM N.A. SUZURI M.; SUZURI M.; SUBMITTED (JAN-2003) to the EMBL/GenBank/DDBJ databases. I2] SEQUENCE FROM N.A. SUZURI M.; SUZURI M.; SUBMITTED (JAN-2003) to the EMBL/GenBank/DDBJ databases. I2] SEQUENCE FROM N.A. SUZURI M.; SUBMITTED (JAN-2003) to the EMBL/GenBank/DDBJ databases. I2] SEQUENCE FROM N.A. SUZURI M.; SUBMITTED (JAN-2003) to the EMBL/GenBank/DDBJ databases. I2] SEQUENCE FROM N.A. SUZURI M.; SUBMITTED (JAN-2003) to the EMBL/GenBank/DDBJ databases. I2] SUBMITTED (JAN-2003) to treamport; IEA. GO; GO:000681; F:Cation channel activity; IEA. GO; GO:0006812; P:Cation channel TrpL. InterPro; IPR00812; Crit Channel TrpL. InterPro; IPR00812; TARTED III like. InterPro; IPR00812; TARTED III like. InterPro; IPR00812; TARTED III like. InterPro; IPR00812; Vanil receptor. InterPro; IPR00814; Vanil receptor. INTERPORTER VANIL REPORTER VANIL R	LT 1 76 086YZ6 PRELIMINARY; PRT; 853 AA.

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Mammalia; Eutheria; I
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.

MEDLINE-22107054; PubMed-12077606;

Smith G.D., Gunthorpe M.J., Kelsell R.E., Hayes P.D., Reil
Facer P., Wright J.E., Jerman J.C., Walhin J-P., Ooi L., E
Charles K.J., Smart D., Randall A.D., Anand P., Davis J.B.

"TRPV3 is a temperature-sensitive vanilloid receptor-like
Nature 418:186-190(2002).

EMBL; AJ296305; CAC82937.1; -.

Genew; HGNC:18083; TRPV4.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005261; F:cation channel activity; IEA.
                                                                                                                                                                                                                                                                           Q8NDY7 PRELIMINARY; PRT; 871 AA. Q8NDY7, 01-0CT-2002 (TrEMBLrel. 22, Created) 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Vanilloid receptor-like channel 2.
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Matches 736
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GO; GO:0006812; P:cation transport; IEA.
InterPro; IPR002110; ANK.
InterPro; IPR002111; Cat channel TrpL.
InterPro; IPR008996; Cytok ILL_like.
InterPro; IPR00891; IOn trans.
InterPro; IPR005821; IOn trans.
InterPro; IPR004729; TRPChannel.
InterPro; IPR008347; Vanil_receptor.
InterPro; IPR008347; Vanil_receptor2.
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Pfam; PF00023; Ank; 3.

Pfam; PF00520; Ion trans; 1.

Pfam; PF00520; Ion trans; 1.

PRINTS; PR01761; TRPVRECEPTOR.

PRINTS; PR01769; VRL2RECEPTOR.

PRINTS; PR01769; VRL2RECEPTOR.

SMART; SM00248; ANK; 1.

TIGREAMS; TIGR00870; tr;

PROSITE; PS50088; ANK REPEAT; 1.

PROSITE; PS50088; ANK REPEAT; 1.

PROSITE; PS50297; ANK_REP_REGION; 1.

ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;

Transport
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                                                                                                                                       NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG
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                                                                      LSSLDTCGEBASVLBILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC
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                                                                                                                                                                                                                                                                                 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC
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R Pfam; PF000520; Jon trans; 1.

R PRINTS; PR01415; ANKYERN.

R PRINTS; PR01768; TRPVEECEPTOR.

R PRINTS; PR01769; VRL2RECEPTOR.

R SMART; SM00248; ANK; 3.

R TIGREAMS; TIGREROBF0; trp; 1.

DR PROSITE; PS50088; ANK REPEAT; 1.

DR PROSITE; PS50297; ANK REP REGION; 1.

DR PROSITE; PS50297; ANK REP REGION; 1.

SY ANK REPEAT; Ionic channel; Transmembrane; Transmemb
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Nat. Cell Biol. 2:695-702(2000).

REMBL, AF258465; AAG16127.1; -.

RGO; GO:0016021; C:integral to membrane; NAS.
RGO; GO:0015281; F:nonselective cation channel act
RGO; GO:0015281; F:nonselective cation channel
RINTERPO; IPR002111; Cat channel TrpL.
RINTERPO; IPR008996; Cytok III like.
RINTERPO; IPR008996; Cytok III like.
RINTERPO; IPR008348; Vanil_receptor.
RRINTERPO; IPR008348; Vanil_receptor2.
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Best Local
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Q9HBC0;
01-MAR-2001
01-MAR-2001
01-MAR-2004
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TISSUE-Renal cortex;
MEDLINE-20482174; PubMed=11025659;
Minenmacher K.,
Trian channel that
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Mammalia; Eutheria;
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ALHIAI ERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
                 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNOPHI
                                                                                        TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT
                                                                                                                                                                 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL
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                                                                     TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNWREFINSPFRDIYYRGQT
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Primates;
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Last sequence update)
Last annotation updat
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                                                                                                                                              VSRGSTADLDGLLPFLLTHKKRL
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01-DEC-2001
01-DEC-2001
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Ishibashi
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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RESULT OPERING OF ACT O
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GO; GO:0016021; C:integral to membrane;
GO; GO:0005261; F:cation channel activit;
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0006812; P:cation transport; IEA.
InterPro; IPR002110; ANK.
InterPro; IPR002111; Cat channel TrpL.
InterPro; IPR008111; Cat channel TrpL.
InterPro; IPR008111; Ion trans.
InterPro; IPR008347; Vanil receptor.
InterPro; IPR008347; Vanil receptor.
InterPro; IPR008348; Vanil receptor2.
                          Pfam; PF00023; Ank; 3.

Pfam; PF000520; Ion trans; 1.

Pfam; PF001520; Ion trans; 1.

PRINTS; PR01165; TRPVERECEPTOR.

PRINTS; PR01769; VRL2RECEPTOR.

PRINTS; PR001769; VRL2RECEPTOR.

SMART; SM00248; ANK; 3.

TIGRPAMB; TIGR00870; trp; 1.

PROSITE; PS50088; ANK REPEAT; 1.

PROSITE; PS50297; ANK REPERGION; 1.

ANK repeat; Ion transport; Ionic cha
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01-DEC-2001 (TremBLrel.
01-MAR-2004 (TremBLrel.
Vanilloid receptor like
Transport
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iBdibashi K.;
iBhibashi K
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Primates;
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Matches 736
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                                              Q96RS7 PRELIMINARY; PRT; 803 AA.
Q96RS7,
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Vanilloid receptor-like protein 2.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI TaxID=9606;
[1]
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                                         Name=VRL2;
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                                                                                                                             TVGQVSKESKHIWKLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.2%; Score 736; DB ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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                  Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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RA Derst C., Schafer M.K.;

RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, APZ79673; AAKS9487.1; -.

EMBL, APZ79673; AAKS9487.1; -.

RGO; GO:0005261; F:cation channel activity; IEA.

RGO; GO:0005261; F:cation channel activity; IEA.

RGO; GO:0005812; P:cation transport; IEA.

DR GO; GO:0006812; P:cation transport; IEA.

DR GO; GO:0006812; P:cation transport; IEA.

DR InterPro; IPR002111; Cat channel TrpL.

DR InterPro; IPR008996; Cytok_IL1_like.

DR InterPro; IPR004729; TRPChannel.

DR InterPro; IPR004729; TRPChannel.

DR InterPro; IPR008348; Vanil_receptor.

DR InterPro; IPR008348; Vanil_receptor2.

DR Pfam; PF00023; Ank; 3.

DR Pfam; PF00520; Ion_trans; 1.

DR Pfam; PF00520; Ion_trans; 1.

DR Pfam; PF00520; Ion_trans; 1.

DR PRINTS; PR01769; VRLZEECEPTOR.

DR PRINTS; PR01769; VRLZEECEPTOR.

DR PROSITE; PS50089; ANK; 3.

DR TIGREAMS; TIGR00870; trp; 1.

DR PROSITE; PS50089; ANK; REPEAN; 1.

DR PROSITE; PS50089; ANK; REPEAN; 1.

DR PROSITE; PS50297; ANK_REP_REGION; 1.

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                                                                                                                                                                                                                                                                                                                                             EBASYLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLT
  FLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGETVGQVSKE
                                            ILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQINCTVPTYPSCRDSETFST
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Best Local S
Matches 735
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005261; F:cation chammel activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR002111; Cat channel TrpL.

InterPro; IPR002111; Cat channel TrpL.

InterPro; IPR008996; Cytok IL1 like.

InterPro; IPR008821; Ion trans.

InterPro; IPR008347; Vanil_receptor.

InterPro; IPR008347; Vanil_receptor2.

Pfam; PF00023; Ank; 3.

Pfam; PF00023; Ank; 3.

PFANNTS; PR01768; TRPVRECEPTOR.

R PRINTS; PR01768; TRPVRECEPTOR.

R PROSITE; PS50088; ANK REPEAT; 1.

R PROSITE; PS50088; ANK REPEAT; 1.

R PROSITE; PS50088; ANK REPEAT; 1.

R PROSITE; PS50087; LTP; 1.

R PROSITE; PS50087; LTP; 1.
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01-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, L
01-MAR-2004 (TrEMBLrel. 26, I
Vanilloid receptor-related of
                                                                                                                                                                                                                                                                                                                                                                                                  ANK repeat;
Transport.
SEQUENCE 8
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Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M.,
Sali A., Hudspeth A.J., Friedman J.M., Heller S.;
"Vanilloid receptor-related osmotically activated ci-
candidate vertebrate osmoreceptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
[1]
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                                                                                                          KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
                                                                                                                                                                                     GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN
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                TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT
                                    TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT
                                                                                        KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL
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                                                                                                                                                                                                                                                                                                                                                                                                        98265 MW;
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, Last annotation update)
osmotically activated channel
                                                                                                                                                                                                                                                                                                                        Score 635; DB Pred. No. 0; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                    A86FB6ECC9103C19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      channel; Receptor; Transmembrane;
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InterPro; IPRO02111; Cat_channel TrpL.
InterPro; IPRO02111; Cat_channel TrpL.
InterPro; IPRO08996; Cytok IL1 like.
InterPro; IPR008996; Cytok IL1 like.
InterPro; IPR008941; Ion_trans.
InterPro; IPR008347; Vanil receptor.
InterPro; IPR008348; Vanil receptor2.
Pfam; PF00202; Ank; 3.
Pfam; PF00520; Ion_trans; 1.
PRINTS; PR01768; TRPVRECEPTOR.
PRINTS; PR01768; TRPVRECEPTOR.
PRINTS; PR01768; ANK; 3.
PROSITE; PR01768; ANK, REPEAT; 1.
PROSITE; PS50088; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8NG64;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
OTRPC4beta cation channel.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
TISSUE=Aortic
Xu F., Satoh E
                                                                                                                                                                                                                                                                         TISSUE=Aortic endothelium;
Xu F., Satch E., Iijima T.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB073669; BAC06573.1; - membrane; IEA.
GO; GO:0005261; F:cation channel activity; IEA.
GO; GO:0005261; P:cation transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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TVGQVSKESKHIWKLQ 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence up
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                                                                        MEDLINE-2051388; PubMed=11081638;
X MEDLINE-20513888; PubMed=11081638;
A Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
Sali A., Hudspeth A.J., Friedman J.M., Heller S.;
Sali A., Hudspeth A.J., Friedman J.M., Heller S.;
"vanilloid receptor-related osmotically activated channel (VR-O/)"
C candidate vertebrate osmoreceptor.";
Cell 103:525-535(2000).

I Cell 103:525-535(2000).

R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0004872; Frication channel activity; IEA.
R GO; GO:0004872; Frication transport; IEA.
R GO; GO:0004872; Frication transport; IEA.
R GO; GO:0006812; P:cation transport; IEA.
R GO; GO:0006812; P:cation transport; IEA.
R GO; GO:0006812; P:cation transport; IEA.
R InterPro; IPR002111; Cat channel TrpL.
R InterPro; IPR008996; Cytok_ILl_like.
InterPro; IPR008996; Cytok_ILl_like.
InterPro; IPR008348; Vanil_receptor.
InterPro; IPR008348; Vanil_receptor2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9ERZ8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Vanilloid receptor-related osmotically activated ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Vroac;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9ERZ8
  Pfam; PF00023; Ank; 3.
Pfam; PF00520; Ion trans; 1.
PRINTS; PR01768; TRPVRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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811 AA; 91220 N
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Rodentia;
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384
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RA Derst C., Schafer M.K.;

RA Derst C., Schafer M.K.;

RE Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

REMBL; AF279672; AAK69486.l; -.

REMBL; AF279672; AAK69486.l; -.

REMBL; AF279673; PAY69486.l; -.

REMBL; AF279673; PAY69486.l; -.

REMBL; AF279673; PAY69486.l; -.

REMBL; AF279673; PECALCIUM channel activity; IDA.

REGO; GO:0005034; F:cosmosensor activity; IDA.

REGO; GO:0005034; F:cosmosensory signaling pathway; IDA.

REGO; GO:0007231; P:cosmosensory signaling pathway; IDA.

REGO; GO:0007231; P:cosmosensory signaling pathway; IDA.

REGO; GO:0007031; PECONOTION INFO.

REGO; GO:0007031; PEC
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Matches 181
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TIGRPAMS; TIGR00870; trp; 1.
PROSITE; PS50088; ANK REPERT; 1.
PROSITE; PS50089; ANK REP_REGION; 1.
ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
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SMART; S
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Q91XR5; O1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Vanilloid receptor-like protein 2.

Name=Trpv4; Synonyms=Vrl2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98009 MW;
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RESULT 10
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                                                                                                    Matches
                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                             GO; GO:0005262; F:calcium channel activity; IDA.
GO; GO:0005034; F:commosensor activity; IDA.
GO; GO:0042538; F:tosmmosensor activity; IDA.
GO; GO:0042531; P:cosmmosensory signaling pathway; IDA.
GO; GO:0047344; P:csynlation of response to osmotic £
GO; GO:0030103; P:vasopressin secretion; IMP.
InterPro; IPR002110; ANK.
InterPro; IPR002110; ANK.
InterPro; IPR002111; Cat channel TrpL.
InterPro; IPR008996; Cytok III like.
InterPro; IPR008996; Cytok III like.
InterPro; IPR004729; TRPChannel.
ThearPro; IPR004729; TRPChannel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 112; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wissenbach U., Boedding M., From Trp12, a novel Trp related profess Lett. 485:127-134(2000).
EMBL; AJ296078; CAC20703.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Transient receptor potential protein 12.
                                                                                                                                                                             TIGRPAMS; TIGR0870; trp; 1.

PROSITE; PS50088; ANK REPEAT; 1.

PROSITE; PS50297; ANK REP REGION; 1.

ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
                                                                                                                                                                                                                                                                               Pfam; PF00023; Ank; 3.
Pfam; PF00520; Ion_trans; 1.
                                                                                                                                                                                                                                                                                                        InterPro; IPR008347; Vanil_receptor.
InterPro; IPR008348; Vanil_receptor2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1926945; Trpv4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20547522; PubMed=11094154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Trpv4; Synonyms=Trp12;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9EPK8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9EPK8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transport.
SEQUENCE
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                  302
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                                                                                                   112;
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                                                                                                                                                                                                                                     ; PR01768; TRPVRECEPTOR.; PR01769; VRL2RECEPTOR.
SM00248; ANK; 3.
NYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKC
                                         LHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHIV
                                                             LHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHIV 301
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                                                                                                                                                        871
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                                                                                               15.1%; So larity 100.0%; I Conservative 0;
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                                                                                                                                                        AA;
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                                                                                                                                                       98026 MW;
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                                                                                             ; Score 112; DB
b; Pred. No. 4.5
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Freichel M., protein from
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Pred. No.
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; Mismatches
                                                                                                                                                       5BAC6E33F89CEA05
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                                                                                                             4.5e-102;
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                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                     pathway; IDA.
to osmotic stress;
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kidney.";
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                                                                                                                          Length 871;
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Best Local
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GG; GO:0005034; F:csalcium channel activ.
GG; GO:0005034; F:csalcium channel activity;
GG; GO:0005034; F:csalcium channel activity;
GG; GO:0042538; P:hyperosmotic salinity
GG; GO:0047848; P:regulation of respons
GG; GO:0047848; P:regulation of respons
GG; GO:0047848; P:regulation of respons
GG; GO:0030103; P:vasopressin secretion
InterPro; IPR002111; Cat channel TrpL.
InterPro; IPR008121; Ion trans.
InterPro; IPR00822; Ion trans.
InterPro; IPR008347; Vanil receptor.
InterPro; IPR008347; Vanil receptor.
InterPro; IPR008348; Vanil receptor2.
Pfam; PF00520; Ion trans; 1.
PRINTS; PR01768; TRPVRECEPTOR.
PRINTS; PR01768; TRPVRECEPTOR.
PRINTS; PR01769; VALZRECEPTOR.
PRINTS; PR01769; ANK; 3.
IGREPAMS; TIGR00870; trp: 1.
PROSITE; PS50089; ANK REPEAT; 1.
PROSITE; PS50297; ANK REPEAT; 1.
                                        Q9ES76
Q9ES76;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
OTRPC4 cation channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9EQZ4
Q9EQZ4;
              Mus musculus (Mouse)
                              Name=Trpv4;
                                                                                                                                                                                                                                                                                                                                                        ANK repeat;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suzuki M., Mizuno A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suzuki M., Mizuno A., Kodaira K., Imai M.;
"Impaired pressure sensation in mice lacking TRPV4.";
J. Biol. Chem. 278:22664-22668(2003).
EMBL; AB021875; BAA83731.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22692536; PubMed=12692122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Trpv4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0042538; P:hyperosmotic salinity response; GO:0007231; P:osmosensory signaling pathway; GO:0047484; P:regulation of response to osmot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0030103; P:vasopressin secretion;
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                                                                                                                                                                                     302
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                                                                                                                                                                                                                                                                                                 112;
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                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                        LHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHIV
                                                                                                                                                                                                     NYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTXFVTKMYDLLLLKC 353
                                                                                                                                                                                   NYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKC
                                                                                                                                                                                                                                        LHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHIV
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                                                                                                                                                                                                                                                                                                                                                        871
                                                       1 (TrEMBLrel.
1 (TrEMBLrel.
4 (TrEMBLrel.
Metazoa;
                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                 Conservative
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Rodentia;
  Chordata;
                                                                                                                                                                                                                                                                                                                                                        98060 MW;
                                                                                                                                                                                                                                                                                                              15.1%;
                                                        16,
26,
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16,
26,
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W; 3285AE576D32DD95
                                                        Last sequence update)
Last annotation updat
                                                                                    Created)
                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                            Score 112; DB 2; L
Pred. No. 4.5e-102;
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Last annotation update)
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  Craniata; Vertebrata; Euteleostomi;
                                                                                                                PRT;
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QSERZ

ID QSERZ

AC QSERZ

AC QSERZ

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DT 01-MA

DT 01-MA

DT 01-MA

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DT 01-MA

DT Wanil

GN Wasme

OC Eukar

OC Mamma

OC Mamma

OC MICH

CO TISSUU

RX MEDLI

RA Liedt

RA Sali

RT Cendi

RT Cendi

RT Cendi

RT Cendi;
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Best Local (
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Nat. Cell Biol. 2:695-702(2000).
RMB1; AF208026; AAG17543.1; -.
MGD; MGI:1926945; Trpv4.
GO; GO:0005262; F:calcium channel activity; IDA.
GO; GO:0005262; F:calcium channel activity; IDA.
GO; GO:0005263; F:osmosensor activity; IDA.
GO; GO:0007231; P:osmosensory signaling pathway; IDA.
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Pfam; PF00520; Ion trans; 1.

PRINTS; PR01768; TRPVRECEPTOR.

PRINTS; PR01769; VKL2RECEPTOR.

SMART; SM00248; ANK; 3.

TIGRPAMs; TIGR00870; trp; 1.

TIGRPAMs; TIGR00870; trp; 1.

PROSITE; PS50088; ANK REPEAT; 1.

PROSITE; PS50087; ANK REPEAT; 1.

ANK repeat; Ion transport; Ionic Channel; Transmembrane; Transport.
                                                                                                                                                                                                                                                                          Q9ERZ7 PRELIMINARY; PRT; 8/3 AA.
Q9ERZ7;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Vanilloid receptor-related osmotically activated channel.
Name=Trpv4; Synonyms=Vroac;
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InterPro; IPR002111; Cat channel TrpL.

InterPro; IPR008996; Cytok III like.

InterPro; IPR008921; Cytok III like.

InterPro; IPR00821; Ion trans.

InterPro; IPR004729; TRPChannel.

InterPro; IPR008347; Vanil_receptor.

InterPro; IPR008348; Vanil_receptor2.
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NCBI TaxID=10090;
                                   TISSUE=Hypothalamus;
MEDLINE=20531888; PubMed=11081638;
Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis Sali A., Hudspeth A.J., Friedman J.M., Heller S.;
"Vanilloid receptor-related osmotically activated channel candidate vertebrate osmoreceptor.";
Cell 103:525-535(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20482174; PubMed=11025659;
Strotmann R., Harteneck C., Nunnenmacher K., Schultz G., Plant T.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=129/SVEV
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                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                    Mammalia; Eutheria;
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                     103:525-535(2000)
; AF263522; AAG280
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   MGI:1926945;
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                       AAG28028.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98069 MW;
                                                                                                                                                                                                                                    Rodentia;
                                                                                                                                                                                                                                                    Chordata;
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                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                   channel (VR-OAC),
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Best Local S
Matches 112
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Pfam; PF000520; Ion trans; 1.

PRINTS; PR011415; ANKYRIN.

PRINTS; PR01768; TRPVRECEPTOR.

PRINTS; PR01769; VRL2RECEPTOR.

SMART; SM00248; ANK; 3.

TIGRFAMS; TIGR00870; ttp; 1.

PROSITE; PS50088; ANK REPEAT; 1.

PROSITE; PS50297; ANK REP REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9DFS3;
                                                                                                                                                                                                                                            MEDLINE-20531888; PubMed=11081638; Liedtke W., Choe Y., Marti-Renom M.A., Bell A.M., Hudspeth A.J., Friedman J.M., Heller S.; "Vanilloid receptor-related osmotically activated candidate vertebrate osmoreceptor."; Cell 103:525-535 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, Vanilloid receptor-related c Name=VR-OAC;
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InterPro; IPR008347; Vanil_recep
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InterPro; IPR002111; Cat channel TrpL.
InterPro; IPR008996; Cytok IL1 like.
InterPro; IPR005821; Ion_trans.
                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
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                         InterPro;
InterPro;
                                                                 InterPro; IPR002110; ANK.
InterPro; IPR002111; Cat_
InterPro; IPR008996; Cyto
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interPro; IPR008348; Vanil_receptor2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
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GO:0042538; P:hyperosmotic salinity response; IMP.
GO:0042531; P:osmosensory signaling pathway; IDA.
GO:0047484; P:regulation of response to osmotic stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0030103; P:vasopressin secretion; IMP.
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GO: 0005034;
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112; Conserv
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                         IPR005821;
IPR002016;
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Conservative
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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  Ribosomal_S2
                                                                 Cytok_IL1_like.
                              Peroxidase.
                                                 Ion_trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Last sequence update)
, Last annotation update)
osmotically activated channel
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Pred. No. 4.5e-102;
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P SEQUENCE.

C TISSUBE-Kidny;

X MEDLINE-99156912; PubMed=10037722;

& Suzuki M., Sato J., Kutsuwada K., Ooki G., Imai M.;

& Suzuki M., Sato J., Kutsuwada K., Ooki G., Imai M.;

& Suzuki M., Sato J., Xutsuwada K., Ooki G., Imai M.;

& Suzuki M., Sato J., Xutsuwada K., Ooki G., Imai M.;

& Suzuki M., Sato J., Xutsuwada K., Ooki G., Imai M.;

& Suzuki M., Sato J., Xutsuwada K., Ooki G., Imai M.;

& Suzuki M., Sato J., Xutsuwada K., Ooki G., Imai M.;

& Toloning of a stretch-inhibitable nonselective cation can

End J. Biol. Chem. 274.6330-6335(1999).

BR GO; GO:0016021; F:cation channel activity; IEA.

DR GO; GO:0006812; P:cation channel TrpL.

DR GO; GO:0006812; P:cation transport; IEA.

DR InterPro; IPR002111; ANK.

DR InterPro; IPR002111; Cat channel TrpL.

DR InterPro; IPR008996; Cytok III_like.

DR InterPro; IPR008996; Cytok III_like.

DR InterPro; IPR008347; Vanil receptor.

Pfam; PF00520; Ion trans; I.

DR PRINTS; PR01768; TRPNECEPTOR.

DR SMART; SM00248; ANK; 1.

DR SMART; SM00248; ANK; 1.
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                                                            Query Match
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Matches 28
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InterPro; IPR008
InterPro; IPR008
InterPro; IPR008
Pfam; PF00023; I
Pfam; PF000520; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9Z182 PRELIMINARY; PRT; 528 AA.
Q9Z182;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 12, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Stretch-inhibitable nonselective channel (SIC).
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SEQUENCE
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PRINTS; PRO1768; TRPVRECEPTOR.

PRINTS; PRO1768; ANK; 3.

SMART; SM00248; ANK; 3.

TIGRFAMS; TIGR00870; trp; 1.

PROSITE; PS50288; ANK REPEAT; 1.

PROSITE; PS50297; ANK REPEAT; 1.

PROSITE; PS00436; PEROXIDASE 2; UNKNOWN 1.

PROSITE; PS00962; RIBOSOMAL_$\frac{32}{21}$; UNKNOWN 1.

PROSITE; PS00962; RIBOSOMAL_$\frac{32}{21}$; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
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                709 LLLNMLIALMGETVGQVSKESKHIWKLQ 736
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                                                                             Similarity
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LLLNMLIALMGETVGQVSKESKHIWKLQ 393
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IPR008347; Vanil_receptor.
IPR008348; Vanil_receptor2.
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                                                              Conservative
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/ 100.0%; Pr
/ 've 0;
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100.0%; Pr
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                                                            ; Score 28; DB
k; Pred. No. 2.1
0; Mismatches
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Sciurognathi; Muridae; Murinae; Rattus.
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                                                                             DB 2;
2.1e-1
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                                                                          .1e-18;
                                                                                                                                         Transport.
                                                                                            Length 528;
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Search completed: December 2, 2004, 22:42:47 Job time : 206 secs

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Maximum DB
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Perfect score:
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seq length: 2000000000
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Query
Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-197-636-8
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US-09-350-457A-2	US-09-252-991A-30631	US-09-252-991A-20010	US-09-252-991A-17357	US-09-583-110-3811	US-09-107-532A-5998	US-09-252-991A-26243	US-08-986-304-3	US-09-252-991A-16650	US-09-248-796A-27147	US-09-248-796A-24245	US-09-134-000C-4066	US-09-270-767-42187	US-08-858-207A-515	US-09-248-796A-26822	US-09-252-991A-24452	US-09-978-303-15	US-09-235-451-15
Sequence 2, Appli	Sequence 30631, A	Sequence 20010, A	Sequence 17357, A	Sequence 3811, Ap	Sequence 5998, Ap	Sequence 26243, A	Sequence 3, Appli	Sequence 16650, A	Sequence 27147, A	Sequence 24245, A	Sequence 4066, Ap	Sequence 42187, A	Sequence 515, App	Sequence 26822, A	Sequence 24452, A	•	Sequence 15, Appl

## ALIGNMENTS

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301 VNYLTENPHKKADMRRQOSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFEDS 360	301 VNYLTENPHKKADMRRQDSRGNTVLHALVALADNTRENTKFVTKMYDLLLLKCARLFPDS 360	241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300	241 ALHIAIERRCKHYVELIVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSIAACTNQPHI 300	181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240	181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240	121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180	121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFILTHKKRL 180	61 GDGRPNIRHKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120	61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGGPKKAPMDSLFDYGTYRHHSSDN 120	1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60	1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60	Query Match 100.0%; Score 742; DB 4; Length 742; Best Local Similarity 100.0%; Pred. No. 0; Matches 742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	WESULT 1  US-09-500-123-12  Sequence 12, Application US/09500123  Patent No. 6455278  GENERAL INFORMATION:  APPLICANT: Dubin, Adrienne E  APPLICANT: Erlander, Mark G  APPLICANT: Erlander, Mark G  APPLICANT: Glass, Charles A  TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor FILE DF INVENTION: VR3  FILE EFFERENCE: Human VR3 receptors FILE REFERENCE: Human VR3 receptors CURRENT APPLICATION NUMBER: US/09/500,123  CURRENT PILING DATE: 2000-02-08  NUMBER OF SEQ ID NOS: 17  SEQ ID NO 12  LENCTH: 742  TYPE: PRT  ORGANISM: Homo sapiens  US-09-500-123-12

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TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor TITLE OF INVENTION: VR3
FILE REFERENCE: Human VR3 receptors
CURRENT APPLICATION UNMBER: US/09/500,123
CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 871
TYPE: PRT
ORGANISM: Homo sapiens
US-09-500-123-7
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dubin, Adrienne E
APPLICANT: Huvar, Arne
APPLICANT: Erlander, Mark G
APPLICANT: Glass, Charles A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSLFIDGSPQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMVIFTLTA YYQPLEGTP PYPYRTTVD YLRLAGEVITL FTGVL FFFTNIKDL FMKKCPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC
                                                                                                                                                                                  GDGRPNLRMKFQCAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
                                                                                                                                                                                                                                           MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP
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ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
                                                              TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT
                                                                                                                         KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
                                                                                                                                                                  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN
                                                                                                                                                                                                                             MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP
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                                                                                                       KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL
                                                                                                                                                                                                                                                                                    85.6%;
nilarity 99.9%;
Conservative
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Pred. No. 0;
0; Mismatches
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RESULT 3
US-09-500-123-9
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Best Local S
Matches 383
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APPLICANT: Huvar, Arne
APPLICANT: Erlander, Mark G
APPLICANT: Erlander, Mark G
APPLICANT: Class, Charles A
TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
TITLE OF INVENTION: VR3
FILE REFERENCE: Human VR3 receptors
CURRENT APPLICATION NUMBER: US/09/500,123
CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 17
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 811
TYPEE. PRET
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                                                                                                                                                                        tch 51.6%; Score 383; DE al Similarity 100.0%; Pred. No. 0; 383; Conservative 0; Mismatches
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                                                          GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN
                                                                         GDGRENLRMKFQGAFRKGVENPIDLLESTLYESSVVPGFKKAPMDSLFDYGTYRHHSSDN 120
                                                                                                                   MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP
                                                                                                                                  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP
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CURRENT APPLICATION NUMBER: US/09/235,451
CURRENT FILING DATE: 199-01-22
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
SECTIANCE: PASTESEQ for Windows Version 3.0
SEC ID NO 2
LENGTH: 838
                                                                                                                                                                                                                                                                                                                    US-09-235-451-2
; Sequence 2, Application US/09235451
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; F
Matches 16; Conservative 0;
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LENGTH: 511
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OTHER INFORMATION: TM1
NAME/KEY: TRANSMEM LOCATION: (480)...(495)
OTHER INFORMATION: TM2
                                                                                                                                                                                        APPLICANT: Julius, David J.
APPLICANT: Caterina, Michael J.
APPLICANT: Brake, Anthony J.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
TITLE OF INVENTION: POLYBEFTIDES AND USES THEREOF
FILE REFERENCE: 9076/084CIP
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CURRENT APPLICATION NUMBER: US/09/667,422
CURRENT FILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 13
SOFTMARE: Patentin Ver. 2.0
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APPLICANT: Krause, James
TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
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Pred. No.
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                                                                ORGANISM: Rattus sp.
PUBLICATION INFORMATION:
AUTHORS: Caterina, Michael J.
AUTHORS: Schumacher, Mark A.
AUTHORS: Tominaga, Makoto
AUTHORS: Tominaga, Makoto
AUTHORS: Rosen, Tobias A.
TITLE: The capsaicin receptor: a
TITLE: the pain pathway
                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 838
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09667422 Patent No. 6482611
                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/667,422
CURRENT FILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cortright, Daniel
APPLICANT: Krause, James
TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
FILE REFERENCE: HCR
JOURNAL: Nature
VOLUME: 389
PAGES: 816-824
DATE: 1997
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APPLICANT: Young, Paul E.

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Vanilloid Receptor-2

FILE REFERENCE: 1488.1110000

CURRENT APPLICATION NUMBER: US/09/132,316B

CURRENT FILING DATE: 1998-08-11

FEARLIER APPLICATION NUMBER: US 60/040,163

EARLIER FILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-03-06

NUMBER OF SEQ ID NOS: 67

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 838

TYPE: PRT

ORGANISM: Rattus norvegicus
                                                                                                                                 US-09-132-316-3
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US-09-132-316-3
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                                                               Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                    282 FYFGELPLSLAACTNQ 297
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                                                               l Similarity
16; Conserv
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1 Similarity 100.0*; Pred. No. 4.6e-07;
16; Conservative 0; Mismatches 0;
FYFGELPLSLAACTNO 260
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                                                            2.2%; Score 16;
100.0%; Pred. No.
tive 0; Mismatcl
                                                               Mismatches
                                                                                             DB 4;
                                                                               4.6e-07;
                                                                                             Length 838;
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                                                              Gaps
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Sequence 2, Application US/099
PATENT NO. 6790629
GENERAL INFORMATION:
APPLICANT: Julius, David J.
APPLICANT: Caterina, Michael
APPLICANT: Brake, Anthony J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-978-303-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-667-422-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-197-636-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: R. rattus
US-09-978-303-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09197636 Patent No. 6239267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                    COUNTRY: US
COUNTRY: US
ZIP: 19482-0980
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: DOS
                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: DUCKWORTH, DAV
APPLICANT: HAYES, PHILIP
APPLICANT: MEADOWS, HELER
APPLICANT: DAVIS, JOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/978,303
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/235,451
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR APPLICATION NUMBER: 08/915,461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic acid sequences encoding
TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
TITLE OF INVENTION: polypeptides and uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: UCAL084CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 838
                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         APPLICANT: MEADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: E
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                                                                                                                                                                       CITY: Valley Forge
STATE: PA
                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                              ADDRESSEE: Ratner & Prestia
APPLICATION NUMBER: US/09/197,636
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                                                                                                                                                                                                                                                                                                                                                                        DUCKWORTH, DAVID
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100.0%; Pred. No.
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Pred. No.
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hes 0;
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RESULT 10
US-09-197-636-4
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                                                                                                                                                                                                                                                                                             Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/197.6°

FILING DATE: 23-NOV-1998

CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION:
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FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 21-JUL-1998
APPLICATION NUMBER: UK 9819278.4
FILING DATE: 03-SER-1998
ATTORNEY, AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-30075
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF THE PROBLEM OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Appl
Patent No. 62392
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Best Local Similarity
                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9805137.8
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 21-JUL-1998
APPLICATION NUMBER: UK 9819278.4
FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION NUMBER: 1
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP
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P.O. Box 980
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DAVIS, JOHN
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          GP-30075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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, MOLECULE TYPE: US-09-197-636-8
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Patent No. 6239267
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Best Local Similarity 100.0%;
Matches 16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: DUCKWORTH, DAVID
APPLICANT: HAYES, PHILLP
APPLICANT: MEADOWS, HELEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO:
                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FASTSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/197,636 FILING DATE: 23-NOV-1998 CLASSIFICATION: PRIOR ADDITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 839 amino acids
TYPE: amino acid
                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 839 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                             REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-407-0700
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                          FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MEADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: F.C. CTTY: Valley Forge
                                                                                                                                                                                                                                                                         FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 21-7UL-1998
APPLICATION NUMBER: UK 9819278.4
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 601-1.
TELEPHONE: 601-1.
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                                 TOPOLOGY:
                                               STRANDEDNESS:
                                                                                                                                               TELEFAX:
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                                                                                                                                                                                                                              Prestia, Paul F
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                                                                                                                                846169
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                            linear
                                                                                                                                               610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss: single
linear
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Pred. No. 4.7e-07
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; SOFTWARE: PatentIn Ver. 1.30
; SEQ ID NO 2
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-533-220A-2
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                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Mcintyre, Peter
APPLICANT: James, Tain Fraser
TITLE OF INVENTION: Human Vanilloid Receptor
FILE REFERENCE: 4-30875A
CURRENT APPLICATION NUMBER: US/09/533,220A
CURRENT FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
PRIOR FILING DATE: 1999-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 34
LENGTH: 839
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34, Application US/09235451 GENERAL INFORMATION:
                                                                 Query Match
Best Local Similarity
Matches 16; Conserv
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Best Local
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Best Local Similarity 100.0%;
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PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Julius, David J.
APPLICANT: Caterina, Michael J.
APPLICANT: Brake, Anthony J.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 9076/084CIP
CURRENT APPLICATION NUMBER: US/09/235,451
CURRENT FILING DATE: 1999-01-22
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 FYFGELPLSLAACTNQ 297
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                  282 FYFGELPLSLAACTNQ 297
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246 FYFGELPLSLAACTNQ 261
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                                                               2.2%; So ilarity 100.0%; I Conservative 0;
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Pred. No.
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RESULT 14 US-09-667-422-4

Sequence 4, Application US/09667422
Patent No. 6482611
GENERAL INFORMATION:

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NAME/EXT: TRANSMEM
LOCATION: (434)..(455)
OTHER INFORMATION: TM1
NAME/EXT: TRANSMEM
LOCATION: (440)..(455)
OTHER INFORMATION: TM2
NAME/EXT: TRANSMEM
LOCATION: (540)..(560)
OTHER INFORMATION: TM3
NAME/EXT: TRANSMEM
LOCATION: (540)..(569)
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NAME/EXT: TRANSMEM
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OTHER INFORMATION: TM6
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LOCATION: (578)...(684)
LOCATION: (57
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Search completed: December Job time : 44 secs

2, 2004, 22:55:04

APPLICANT: Cortright, Daniel
APPLICANT: Krause, James
ITITE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
FILE REFERENCE: HCR
CURRENT APPLICATION NUMBER: US/09/667,422
CURRENT FILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 839
TYPE: PRT
ORGANISM: Homo sapiens

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Maximum DB
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Perfect score:
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seq length: 2000000000
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6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No.	Score	Match Length DB	ength		ID	Description
1	742	100.0	742	14	US-10-090-215-12	Sequence 12, Appl
2	736	99.2	831	15	US-10-342-844-76	
ω	736	99.2	870	16	US-10-761-065-2	2
4	736	99.2	871	10	US-09-870-090-2	Sequence 2, Appli
ഗ	736	99.2	871	14	US-10-000-823-7	7
ō,	736	99.2	871	14	US-10-171-319-17	Sequence 17, Appl
7	736	99.2	871	15	US~10-342-844-54	54
80	736	99.2	871	15	US-10-342-844-58	Sequence 58, Appl
9	736	99.2	871	15	US-10-342-844-78	78
10	736	99.2	871	17	US-10-415-570A-2	Sequence 2, Appli
11	668	90.0	803	15	US-10-342-844-56	Sequence 56, Appl
12	635	85.6	871	14	US-10-027-828-2	2
13	635	85.6	871	14	US-10-027-828-4	Sequence 4, Appli

## ALIGNMENTS

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US-10-090-215-12
; Sequence 12, Application US/10090215
; Publication No. US20030032097A1
                                                                                                                                                                                                                                                                                                        US-10-090-215-12
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor TITLE OF INVENTION: VR3
FILE REFERENCE: Human VR3 receptors
CURRENT APPLICATION NUMBER: US/10/090,215
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 742
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                       Matches 742; Conservative
                                                                                                                                                                                                                                        Query Match 100.0%; Score 742; Best Local Similarity 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dubin, Adrienne E
APPLICANT: Huvar, Arne
APPLICANT: Erlander, Mark G
APPLICANT: Glass, Charles A
121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
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                                                                                   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
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                                                              GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN
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Erlander, Mark G
Glass, Charles A
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APPLICANT: ROOS, Jack
APPLICANT: Stauderman, Kenneth
APPLICANT: Velicelebi, G"n 1
APPLICANT: Velicelebi, G"n 1
TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCI)
FILE REFERENCE: 37481-3307
CURRENT APPLICATION NUMBER: US/10/342,844
CURRENT FILING DATE: 2003-01-11
PRIOR APPLICATION NUMBER: US 60/347,459
PRIOR APPLICATION NUMBER: US 60/347,459
PRIOR APPLICATION NUMBER: US 60/401,171
PRIOR APPLICATION NUMBER: US 60/401,171
PRIOR APPLICATION NUMBER: US 60/405,678
PRIOR APPLICATION NUMBER: US 60/405,678
PRIOR FILING DATE: 2002-08-02
PRIOR FILING DATE: 2002-08-20
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 76
LENGTH: 831
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 76, Application US/10342844
Publication No. US20040009537A1
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
NAME/KEY: VARIANT
LOCATION: 804, 816
OTHER INFORMATION: Xaa = Any Amino
PUBLICATION INFORMATION:
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Sequence 2, Application US/10761065

Publication No. US20040137573A1

JENERAL INFORMATION:
APPLICANT: Pfizer, Inc.
APPLICANT: Katsuhiro Shinjo
APPLICANT: Katsuhiro Shinjo
APPLICANT: Hikaru Yabuuchi
TITLE OF INVENTION: Human Vanilloid Receptor-Like ProFILE REFERENCE: PC9979ADAM
CUURRENT APPLICATION NUMBER: US/10/761,065
CUURRENT FILING DATE: 2004-01-20
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; DATABASE ENTRY DATE: 2001-10-16
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RESULT 4
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ORGANISM: Human
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GENERAL INFORMATION:

APPLICANT: Pfizer Product Inc.

TITLE OF INVENTION: Human Vanilloid Receptor-Like Profile Reference: pc979A

CURRENT APPLICATION NUMBER: US/09/870,090

CURRENT FILLING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: US 60/208,156

PRIOR APPLICATION NUMBER: US 60/208,156

PRIOR FILING DATE: 2000-05-31

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 871

TYPE: PAT

CRGANISM: Human

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RESULT 5
US-10-000-823-7
(Sequence 7, Application US/10000823
; Sequence 7, Application US/10000823
; Publication No. US20030027164A1
; GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING A NO TITLE OF INVENTION: HUMAN ION CHANNEL EXPRESSED IN SPINAL CORD AND BRAIN
; FILE REFERENCE: D0109NP
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; ORGANISM: Homo sapiens
US-10-000-823-7
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CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/250,587
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.2%; Score 736; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 736; Conservative 0; Mismatches
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                                                                                   TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC
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; ORGANISM: Homo
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US-10-171-319-17
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CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 60/297,835
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/351,238
PRIOR FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/352,914
PRIOR PILING DATE: 2002-01-29
PRIOR PILING DATE: 2002-01-29
PRIOR PILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: 60/357,161
PRIOR APPLICATION NUMBER: 60/357,161
PRIOR APPLICATION NUMBER: 60/381,086
PRIOR APPLICATION NUMBER: 60/381,086
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-15
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SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 871
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Publication No.
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TITLE OF INVENTION: VANILLOID RECEPTOR-RELATED NUCLEIC ACIDS
TITLE OF INVENTION: AND POLYPEPTIDES
FILE REFERENCE: 4-32048A
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                      NLEAVLANDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD
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APPLICANT: Standerman, Kenneth
APPLICANT: Velicelebi, G"n |
FITLE OF INVENTION: MCHODULATING AND IDENTIFYING
FITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
FILE REFERENCE: 37481-3307
CURRENT APPLICATION NUMBER: US/10/342,844
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US 60/347,459
PRIOR FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/401,171
PRIOR APPLICATION NUMBER: US 60/401,171
PRIOR APPLICATION NUMBER: US 60/405,678
PRIOR FILING DATE: 2002-08-02
PRIOR FILING DATE: 2002-08-20
                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 54
LENGTH: 871
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2002-09-01
US-10-342-844-54
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Best Local Similarity
Matches 736; Conser
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Publication No. US20040009537A1
GENERAL INFORMATION:
APPLICANT: Roos, Jack
APPLICANT: Stauderman, Kenneth
APPLICANT: Velicelebi, G"n_1
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APPLICANT: Velicelebi, G"n 1
FITTLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
FITTLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCI
CURRENT APPLICATION NUMBER: US/10/342,844
CURRENT APPLICATION NUMBER: US/0347,459
PRIOR APPLICATION NUMBER: US 60/347,459
PRIOR APPLICATION NUMBER: US 60/401,171
PRIOR APPLICATION NUMBER: US 60/401,171
PRIOR APPLICATION NUMBER: US 60/405,678
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 115
SOFTMARE: FastSEQ for Windows Version 4.0
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US-10-342-844-58
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              Query Match
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Matches 736;
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Publication No. US20040009537A1
                                                                                                  LENGTH: 871
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genb.
DATABASE ENTRY DATE: 2001-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Roos, Jack
APPLICANT: Staudermar
APPLICANT: Velicelebi
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                  Conservative
         99.2°,
100.0%; Pi
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                             Score 736; ; Pred. No.
                Mismatches
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APPLICANT: Standerman, Kenneth
APPLICANT: Velicelebi, G"n.
TITLE OF INVENTION: METHODS OF MODULATING AN
TITLE OF INVENTION: AGENTS THAT MODULATE IN
THAT APPLICATION NUMBER: US/10/342,844
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US 60/401,171
PRIOR APPLICATION NUMBER: US 60/401,171
PRIOR APPLICATION NUMBER: US 60/405,678
PRIOR FILING DATE: 2002-08-02
PRIOR FILING DATE: 2002-08-20
NUMBER OF SEQ ID NOS: 115
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TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORWATION:
DATABASE ACCESSION NUMBER: Genbank
DATABASE ENTRY DATE: 2000-09-26
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RESULT 10
US-10-415-570A-2
(Sequence 2, Application US/10415570A
Publication No. US20040198649A1
GENERAL INFORMATION:
APPLICANT: Davis, John Beresford

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CALCIUM

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APPLICANT: SMART, DARYEN
TITLE OF INVENTION: New Use
FILE REFERENCE: 932689
CURRENT APPLICATION NUMBER: US/10/415,570A
CURRENT FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: PCT/GB01/04739
FRIOR APPLICATION NUMBER: GB 0026114.9
FRIOR APPLICATION NUMBER: GB 0026114.9
PRIOR FILING DATE: 2000-10-25
PRIOR FILING DATE: 2000-10-25
UNMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo
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; TYPE: PAT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ENCESSION NUMBER: Genban!
; DATABASE ENTER DATE: 2001-07-02
US-10-342-844-56
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Publication No. US20040009537A1
; GENERAL INFORMATION:
APPLICANT: Roos, Jack
APPLICANT: Stauderman, Kenneth
APPLICANT: Stauderman, Kenneth
APPLICANT: Welicelebi, G"n_1
TITLE OF INVENTION: METHODS OF MODULATING AN
TITLE OF INVENTION: AGENTS THAT MODULATE IN
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US-10-342-844-56
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CURRENT APPLICATION NUMBER: US/10/342,844
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US 60/347,459
PRIOR FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/401,171
PRIOR APPLING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/405,678
PRIOR APPLICATION NUMBER: US 60/405,678
PRIOR FILING DATE: 2002-08-20
PRIOR FILING DATE: 2002-08-20
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 56
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Best Local :
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                                 FQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQK
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APPLICANT: Liedtke, Wolfgang
APPLICANT: Heller, Stefan
APPLICANT: Hudspeth, Albert J.
APPLICANT: Hudspeth, Albert J.
APPLICANT: Friedman, Jeffrey M.
ITILE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACID:
ITILE OF INVENTION: IT, AND USES THEREOF
ITILE OF INVENTION INDEER: US/10/027,828
CURRENT APPLICATION NUMBER: US/10/027,828
CURRENT APPLICATION NUMBER: US/60/243,568
PRIOR APPLICATION NUMBER: US 60/243,568
PRIOR APPLICATION NUMBER: US 60/243,568
PRIOR FILING DATE: 2000-10-26
NUMBER: OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 871
TYPE: PRT
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Matches
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ORGANISM: Homo sapiens
-10-027-828-2
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                       LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC
                                                                 NLEAVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD
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US-10-027-828-4
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APPLICANT: Liedtke, Wolfgang
APPLICANT: Heller, Stefan
APPLICANT: Hudspeth, Albert J.
APPLICANT: Hudspeth, Albert J.
APPLICANT: Friedman, Jeffrey M.
TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACIDS
TITLE OF INVENTION: IT, AND USES THEREOF
FILE REFERENCE: 600-1-287N
CURRENT APPLICATION NUMBER: US/10/027,828
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 60/243,568
PRIOR APPLICATION NUMBER: US 60/243,568
PRIOR PILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Attentin version 3.1
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Best Local Similarity 99.5
Matches 735; Conservative
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                                                                                        ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
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   VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS
                                                                      ALHIVIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI
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99.9%;
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Pred. No. 0;
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Sequence 7, Application US/10090215

; Publication No. US20030032097A1

; GENERAL INFORMATION:
   APPLICANT: Dubin, Adrienne E
   APPLICANT: Dubin, Adrienne E
   APPLICANT: Erlander, Mark G
   APPLICANT: Glass, Charles A
   TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
   TITLE OF INVENTION: VR3
   FILE REFERENCE: Human VR3 receptors
   CURRENT APPLICATION NUMBER: US/10/090,215
   CURRENT FILING DATE: 2002-03-04
   NUMBER OF SEQ ID NOS: 17
   SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                         ; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo s
US-10-090-215-7
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US-10-090-215-7
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APPLICANT: Velicelebi, G"n_1
ITITLE OF INVENTION: METHODS OF MODULATING ANI
ITITLE OF INVENTION: ACENTS THAT MODULATE IN
FILE REFERENCE: 37481-3307
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US/10/342,844
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/347,459
PRIOR FILING DATE: 2002-01-11
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 115
SEQ ID NO 60
TENCTH: 871
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Publication No. US20040009537A1
                                                                               Best Local Sir
Matches 735;
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                                                                                                             Query Match
                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AAG28029
DATABASE ENTRY DATE: 2000-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Roos, Jack
APPLICANT: Stauderman
APPLICANT: Veliceleb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  736
                                                                             Score 635; DB Pred. No. 0; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND IDENTIFYING INTRACELLULAR C.
                                                                                                             DB
                                                                             1;
                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALCIUM
```

0;

Gaps

0

		721 TVGC	
	TVGOVSKESKHIWKLO 736	721	
720	RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE	661	
720	RDSETFSTFLLDLFXLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLIMLIALMGE	661	
660	TYSIMIQKILEKOLFRELLVYLLEMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC	601	
660	TYSIMIQKILEKDLERELLVYLLEMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC	601	
600	NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGMMNALYFTRGLKLTG	541	
600	NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGMMVALYFTRGLKLTG	541	
540		481	
540	AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV	481	
480	LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC	421	
480	LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC	421	
420	NLEAVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD	361	
420		361	
360	VNYLTENPHKKADMRRQDSRGNTVLHALVALADNTRENTKFVTKMYDLLLLKCARLFPDS	301	
360	- (X)	301	
300	ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELFLSLAACTNQPHI	241	
300		241	
240	TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT	181	
240		181	
180	KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL	121	
180		121	
120	GDGRPNLRMKFQGAFRKGVPNFIDLLESTLYESSVVPGPKKAFMDSLFDYGTYRHHSSDN	61	
120		61	

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